

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 6, 2005, 12:28:42 ; Search time 5374.67 Seconds  
(without alignments)  
10403.867 Million cell updates/sec

Title: US-09-904-584-2  
Perfect score: 1154  
Sequence: 1 atggactcccgatccagat.....ccagatgactagtcgtgga 1154

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb.ba.\*

2: gb.htg.\*

3: gb.in.\*

4: gb.on.\*

5: gb.ov.\*

6: gb.pat.\*

7: gb.ph.\*

8: gb.pl.\*

9: gb.pr.\*

10: gb.ro.\*

11: gb.sts.\*

12: gb.sy.\*

13: gb.un.\*

14: gb.vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1152.4	99.9	1154	9	HSU17298 Human kappa
2	1152.4	99.9	1179	6	CQ723157 Sequence
3	1152.4	99.9	1604	9	HUMOPRK1B
4	1144.4	99.2	1182	6	AR270854 Sequence
5	1144.4	99.2	1182	6	AX548862 Sequence
6	1144.4	99.2	1182	6	AX774764 Sequence
7	1144.4	99.2	1182	9	HSU11053 Human kappa
8	1141.4	98.9	1143	6	AR281679 Sequence
9	1140.4	98.8	1142	6	A48343 Sequence 1
10	1140.4	98.8	1142	6	AR141371 Sequence
11	1138.2	98.6	1143	9	AR498922 Homo sapi
12	1136.2	98.5	1284	6	AR281680 Sequence
13	1130.2	97.9	1143	6	AX280919 Sequence
14	1056.8	91.6	1396	9	AY168006 Homo sapi
15	999.4	86.6	1275	6	AR281681 Sequence
16	994.6	86.2	1275	6	AR281682 Sequence
17	933.8	80.9	1733	10	CFU04092 Cavia porce
18	912.4	79.1	1273	10	RATRORD D16534 Rattus norv
19	912.4	79.1	1358	10	RATRORD L22001 Rat kappa o

20	910.8	78.9	4742	10	RNU00442	U00442 Rattus norv
21	909.2	78.8	1288	10	S81111	S81111 kappa-opioi
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24	909.2	78.8	1410	6	AR105149	AR105149 Sequence
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32	632.2	54.8	757	4	PIGKOR	L49437 Sus scrofa
33	590.2	51.1	715	4	AF012105	AF012105 Sus scrof
34	577	50.0	1941	5	AY725197	AY725197 Taricha g
35	544.4	47.2	179356	2	AC083844	AC083844 Homo sapi
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37	512.2	44.4	1454	5	AF530573	AF530573 Rana pipi
38	489.8	42.4	1477	5	AF285173	AF285173 Danio rer
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## ALIGNMENTS

RESULT 1  
LOCUS HSU17298 1154 bp mRNA linear PRI 14-JUL-1995  
DEFINITION Human kappa opioid receptor (hKOR) mRNA, complete cds.  
ACCESSION U17298  
VERSION U17298.1 GI:596069  
KEYWORDS  
SOURCE Homo sapiens (human)

ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS

TITLE

JOURNAL  
MEDLINE  
PUBMED

REFERENCE  
2 (bases 1 to 1154)

Manesson, E., Bare, L. and Yang, D.

Isolation of a human kappa opioid receptor cDNA from placenta

Biochem. Biophys. Res. Commun. 202 (3), 1431-1437 (1994)

JOURNAL  
MEDLINE  
PUBMED

REFERENCE  
3 (bases 1 to 1154)

Kieffer, B.

Direct Submission

Submitted (18-NOV-1994) Brigitte Kieffer, Ecole Supérieure De

Biotechnologie De Strasbourg, Boulevard Sebastien Brandt, Illkirch,

67400, France

FEATURES

source

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Db	61	TGCTGCCCGCCCAACACAGCGCTGTCTTCCGGCTGGCGGAGCCCGACAGCAACGCG	120		
Qy	121	AGCGCGGCTCGAGGACCGGAGCTGGAGCCCGCACATCTCCCGGCGCATCCCGGTC	180		
Db	121	AGCGCGGCTCGAGGACCGGAGCTGGAGCCCGCACATCTCCCGGCGCATCCCGGTC	180		
Qy	131	AGCGCGGCTCGAGGACCGGAGCTGGAGCCCGCACATCTCCCGGCGCATCCCGGTC	190		
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Qy	181	ATCATCAGCGCGGTCTACTCCGTAGTGTCTGGTGGGCAACTCGTGGTC	240		
Db	181	ATCATCAGCGCGGTCTACTCCGTAGTGTCTGGTGGGCAACTCGTGGTC	240		
Qy	191	ATCATCAGCGCGGTCTACTCCGTAGTGTCTGGTGGGCAACTCGTGGTC	250		
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LOCUS	1179 bp DNA linear				PAT 03-FEB-2004
DEFINITION	Sequence 9091 from Patent WO02068579.				
ACCESSION	CQ723157				
VERSION	CQ723157.1				GI:42284014
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE					
AUTHORS	Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.				
TITLE	Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof				
JOURNAL	Patent: WO 02068579-A 9091 06-SEP-2002; PE Corporation (NY) (US)				
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## RESULT 3

HUMOPRK1B  
LOCUS HUMOPRK1B 1604 bp mRNA linear PRI 22-MAR-1995  
DEFINITION Homo sapiens (clone d2-115) kappa opioid receptor (OPRK1) mRNA,  
complete cds.  
ACCESSION L37362  
VERSION L37362.1 GI:722617  
KEYWORDS OPRK1 gene; kappa opioid receptor; opioid receptor.

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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1604)
AUTHORS Zhu,J., Chen,C., Xue,J.-C., Kunapuli,S., Deriel,J.K. and
Liu-Chen,L.-Y.
TITLE Cloning of a human .kappa. opioid receptor from the brain
JOURNAL Life Sci. 56, 201-207 (1995)
COMMENT Original source text: Homo sapiens (clone d2-115) (tissue library:
genomic in lambda dash and cDNA in lambda ZAPII) fetus brain cDNA
to mRNA.
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## ORIGIN

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RESULT 4  
LOCUS AR270854  
DEFINITION Sequence 1417 from patent US 650938.  
ACCESSION AR270854  
VERSION AR270854.1 GI:29702088  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1182)  
AUTHORS Au-Young, J. and Seilhamer, J.J.  
TITLE Composition for the detection of signaling pathway gene expression  
JOURNAL Patent: US 650938-A 1417 31-DEC-2002;  
FEATURES  
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Db |||||  
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Db 1154 TGACTAGTCGTGGA 1167

RESULT 5
AX548862
LOCUS AX548862 1182 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 147 from Patent WO02061087.
ACCESSION AX548862
VERSION AX548862.1 GI:25813740
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Burmer, G.C., Roush, C.L. and Brown, J.P.
TITLE Antigenic peptides, such as for G protein-coupled receptors
(GPCRs), antibodies thereto, and systems for identifying such
antigenic peptides
JOURNAL Patent: WO 02061087-A 147 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
FEATURES
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Location/Qualifiers
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ORIGIN
Query Match 99.2%; Score 1144.4; DB 6; Length 1182;
Best Local Similarity 99.5%; Pred. No. 3.7e-200;
Matches 1148; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGACTCCCGATCCAGATCTTCGCGGGAGAGCGGCGCTTACTGCGCCCGGAGCGCC 60
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Db 1154 TGACTAGTCGTGGA 1167

RESULT 6
AX774764
LOCUS AX774764 1182 bp DNA linear PAT 09-JUL-2003
DEFINITION Sequence 80 from Patent WO03038129.
ACCESSION AX774764
VERSION AX774764.1 GI:32486280
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Raponi, M.
TITLE Methods for assessing and treating leukemia
JOURNAL Patent: WO 03038129-A 80 08-MAY-2003;
Ortho-Clinical Diagnostics, Inc. (US)
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Query Match 99.2%; Score 1144.4; DB 6; Length 1182;
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QY	61	TGCTCGCCCGCCCAACAGCAGCGCTGGTTTCCGGCTGGCGCGAGCGCGACAGCAACGCG	120
Db	74	TGCTCGCCCGCCCAACAGCAGCGCTGGTTTCCGGCTGGCGCGAGCGCGACAGCAACGCG	133
QY	121	AGCGCGGCTCGGAGGACGCGAGCTGGAGCGCGCGCACATCTCCCGCGCATCCCGGTC	180
Db	134	AGCGCGGCTCGGAGGACGCGAGCTGGAGCGCGCGCACATCTCCCGCGCATCCCGGTC	193
QY	181	ATCATCAGCGCGCTTACTCCGAGTGTGCTGCTGGGCTTGGTGGGCAACTCGCTGGTC	240
Db	194	ATCATCAGCGCGCTTACTCCGAGTGTGCTGCTGGGCTTGGTGGGCAACTCGCTGGTC	253
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Db	254	ATGTTCTGTGATCATCCGATACAAAGATGAAGACAGCAACCAATTTACATATTAAAC	313
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Db	314	CTGGCTTTGGCAGATGCTTTAGTTACTACCAACATGCCCTTTCCAGAGTACGGTCTACTTG	373
QY	361	ATGAATTCCTGGCTTTGGGATGTGCTGCAAGATAGTAATTTCCATTTGATTACTAC	420
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Db	554	TGCATCTGGCTGTGCTGATCTGTTGGATCTCTGCAATAGTCTTGGAGGACCAAA	613
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QY	721	ATCATCATCTGCTACACCTGATGATCTCGGCTCAAGAGCGTTCGGCTCCTTTCT	780
Db	734	ATCATCATCTGCTACACCTGATGATCTCGGCTCAAGAGCGTTCGGCTCCTTTCT	793
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Db	794	GGCTCCCGAGAGAAAGATCCAACTGCTGAGGATCACCAGATGCTGCTGCTGGTGGTG	853
QY	841	GCAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	900
Db	854	GCGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	913
QY	901	AGCACTCCACAGCAGCAGTGTCTTCCAGCTATTTACTTCTGCACTGCTGCTGCTGCT	960
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QY	961	ACCAAGATGAGCTGAATCCATTTCTAGCGCTTTCTTGTATGAAACTTCAAGCGGTGT	1020
Db	974	ACCAAGATGAGCTGAATCCATTTCTAGCGCTTTCTTGTATGAAACTTCAAGCGGTGT	1033
QY	1021	TTCCGGGACTTCTGCTTTTCACTGAAGATGAGGATGAGCGCGAGCAGCACTAGCAGATC	1080

Db	1034	TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGAGCAGACTACGAGATC	1093
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DEFINITION	Human kappa opioid receptor (hKOR) mRNA, complete cds.		
ACCESSION	U11053		
VERSION	U11053.1	GI:532059	
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens		
REFERENCE	Mansson, E., Bare, L. and Yang, D.		
AUTHORS	Isolation of a human kappa opioid receptor cDNA from placenta		
TITLE	Biochem. Biophys. Res. Commun. 202 (3), 1431-1437 (1994)		
JOURNAL	MEDLINE		
PUBMED	8060324		
REFERENCE	Mansson, E.		
AUTHORS	Direct Submission		
TITLE	Submitted (20-JUN-1994) Erik Mansson, Molecular Biology, Ohmeda,		
JOURNAL	PPD, 100 Mountain Avenue, Murray Hill, NJ 07974, USA		
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QY	61	TGCTCGCCCGCCCAACAGCAGCGCTGGTTTCCGGCTGGCGCGAGCGCGACAGCAACGCG	120
Db	74	TGCTCGCCCGCCCAACAGCAGCGCTGGTTTCCGGCTGGCGCGAGCGCGACAGCAACGCG	133
QY	121	AGCGCGGCTCGGAGGACGCGAGCTGGAGCGCGCGCACATCTCCCGCGCATCCCGGTC	180
Db	134	AGCGCGGCTCGGAGGACGCGAGCTGGAGCGCGCGCACATCTCCCGCGCATCCCGGTC	193

Qy	181	ATCATCAGCGCGGTCTACTCGT	AGTGTTCGTCTGGGCTTGGTGGGCAATCGCTCGGT	240
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Qy	241	ATGTTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAAC	300	
Db	254	ATGTTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAAC	313	
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Qy	361	ATGAATTTCTGGCCCTTTTGGGGATGCTGTGCAAGATAGTAATTTTCATTTGATTTACTATC	420	
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Qy	781	GGCTCCCGAGAGAAAGATCCGAACCTGGTAGGATCACCAGACTGGTCTCTGGTGGTGGTG	840	
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DEFINITION Sequence 1 from patent US 6146835.
ACCESSION AR141371
VERSION AR141371.1 GI:15100887
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1142)
AUTHORS Kieffer, B. and Simonin, F.
TITLE Human kappa opioid receptor, nucleic acids and uses thereof
JOURNAL Patent: US 6146835-A 1 14-NOV-2000;
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DEFINITION Homo sapiens opioid receptor kappa (OPRK1) mRNA, complete cds.
ACCESSION AF498922
VERSION AF498922.1 GI:20379019
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SOURCE Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
1 (bases 1 to 1143)
AUTHORS Puhl, H.L., Ikeda, S.R. and Aronstam, R.S.
TITLE Direct Submission
JOURNAL Submitted (05-APR-2002) cDNA Resource Center, Guthrie Research
Institute, One Guthrie Square, Sayre, PA 18840, USA
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CHPVKALDPTPLKAKLINICILWSSVGSIAVLGGTKVREDVDVIECSLQRPDD
YSWDLFMKICVFIFAPVPLIIIVICITLMLILKLSVRLSGSREKDRNRRILRV
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ORIGIN									
Query Match 98.6%; Score 1138.2; DB 9; Length 1143; Best Local Similarity 99.7%; Pred. No. 5e-199; Matches 1140; Conservative 0; Mismatches 3; Indels 0; Gaps 0;									
QY	1	ATGGACTCCCGATTCAGATCTTCCCGGGAGCCGGCCCTACCTGCGCCCGAGCGCC	60						
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QY	61	TGCTGCCCGCCCAACAGCAGCGCTGTTTCCCGCTGGCGGAGCCCGACAGCAACGGC	120						
DB	61	TGCTGCCCGCCCAACAGCAGCGCTGTTTCCCGCTGGCGGAGCCCGACAGCAACGGC	120						
QY	121	AGCGCCGGCTCGGAGGACGCGAGCTGGAGCCCGCGCAATCTCCCGCGCATCCCGGTC	180						
DB	121	AGCGCGGCTCGGAGGACGCGAGCTGGAGCCCGCGCAATCTCCCGCGCATCCCGGTC	180						
QY	181	ATCATCAGCGGCTCTACTCCGTAGTCTTCTGCTGGCTTGGTGGCAACTCGCTGTC	240						
DB	181	ATCATCAGCGGCTCTACTCCGTAGTCTTCTGCTGGCTTGGTGGCAACTCGCTGTC	240						
QY	241	ATGTTCTGTATCATCCGATACAAAGATGAAGACAGCAACCAATTTACATATTAAAC	300						
DB	241	ATGTTCTGTATCATCCGATACAAAGATGAAGACAGCAACCAATTTACATATTAAAC	300						
QY	301	CTGCTTTGGCAGATGCTTTAGTTATCTAACCAATGCTTTCAGAGTACGCTACTTG	360						
DB	301	CTGCTTTGGCAGATGCTTTAGTTATCTAACCAATGCTTTCAGAGTACGCTACTTG	360						
QY	361	ATGAATTCCTGGCTTTGGGATGCTCTGCAAGATAGTAATTTCCATTGATTACTAC	420						
DB	361	ATGAATTCCTGGCTTTGGGATGCTCTGCAAGATAGTAATTTCCATTGATTACTAC	420						
QY	421	AACATGTTTACAGCATCTTCACTTCAACCATGATGAGCGTGACCGCTACATTTGCCGTG	480						
DB	421	AACATGTTTACAGCATCTTCACTTCAACCATGATGAGCGTGACCGCTACATTTGCCGTG	480						
QY	481	TGCCACCCCGTGAAGGCTTTGGACTTCGGCACACCTTTGAAGCAAGATCATCAATATC	540						
DB	481	TGCCACCCCGTGAAGGCTTTGGACTTCGGCACACCTTTGAAGCAAGATCATCAATATC	540						
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QY	601	GTCAGGGAAGACGTCGATGTCATGATGTCCTTTGAGTTCCTCCAGATGATGACTTCC	660						
DB	601	GTCAGGGAAGACGTCGATGTCATGATGTCCTTTGAGTTCCTCCAGATGATGACTTCC	660						
QY	661	TGGTGGGACCTTTCATGAGATCTGGCTCTTCATCTTTGCTTCGTGATCCCTGCTC	720						
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QY	721	ATCATCATCTGCTGTCTACACCTGATGATCTCGGTCTCTCAAGAGCGTCCGCTCTTCT	780						
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QY	781	GGCTCCCGAGAGAAAGATCGCAACCTGGTGAAGATCAGACGTCGTCTGGTGGTGGT	840						
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QY	841	GCAGTCTTCTGCTGCTGGACTCCCATTCACATATTATCTCTGGTGGAGGCTCTGGGG	900						
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SEQUENCE 3 from patent US 6518480.									
AR281680 ACCESSION AR281680									
AR281680.1 GI:29717435									
KEYWORDS Unknown.									
SOURCE ORGANISM Unknown.									
UNCLASSIFIED.									
REFERENCE 1 (bases 1 to 1284)									
AUTHORS Conklin,B.R.									
TITLE Selective target cell activation by expression of a G									
JOURNAL protein-coupled receptor activated superiorly by synthetic ligand									
FEATURES Patent: US 6518480-A 3 11-FEB-2003;									
source location/Qualifiers									
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QY	62	GCCTGCCCGCCCAACAGCAGCGCTGTTTCCCGGCTGGCGGAGCCCGACGACACGCA	121						
DB	173	GCCTGCCCGCCCAACAGCAGCGCTGTTTCCCGGCTGGCGGAGCCCGACGACACGCA	232						
QY	122	GGCGGCTCGGAGGAGCGGAGCTGGAGCCCGCGCACATCTCCCGGCGCATCCCGGTCA	181						
DB	233	GGCGGCTCGGAGGAGCGGAGCTGGAGCCCGCGCACATCTCCCGGCGCATCCCGGTCA	292						
QY	182	TCATCAGCGGCTTACTCCGTAGTCTCGTGGGCTTGGTGGGCAACTCGCTGGTCA	241						
DB	293	TCATCAGCGGCTTACTCCGTAGTCTCGTGGGCTTGGTGGGCAACTCGCTGGTCA	352						
QY	242	TGTTCTGATCATCCGATACACAAAGATGAAGACGACCAACATTTACATATTAAAC	301						
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QY	302	TGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCGCTTTTCAGAGTACGGTCTACTTGA	361						
DB	413	TGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCGCTTTTCAGAGTACGGTCTACTTGA	472						
QY	362	TGAATTCCTGGGCTTTTGGGATGCTCTGTGAGATAGTAAATTTTCATTGATTACTACA	421						
DB	473	TGAATTCCTGGGCTTTTGGGATGCTCTGTGAGATAGTAAATTTTCATTGATTACTACA	532						
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DB	533	ACATGTTTCCAGCATCTTCCCTTCCATGATGAGCGTGGACCGCTACATTTGCCGTGT	592						
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QY 1141 TGA 1143
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Db 1141 TGA 1143

RESULT 14
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LOCUS Homo sapiens DRG kappa 1 splice variant KOR 1A mRNA, complete cds,
DEFINITION alternatively spliced.
ACCESSION AY168006
VERSION AY168006.1 GI:27373027
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1396)
AUTHORS Lu, L.D. and Mansson, E.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-2002) Molecular Biology, Adolor Corporation, 371
Phoenixville Pike, Malvern, PA 19355, USA
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Best Local Similarity 96.2%; Pred. No. 4.5e-184;
Matches 1110; Conservative 0; Mismatches 2; Indels 42; Gaps 1;

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QY 121 AGCGCGCGGCTCGGAGGACGCGCAGCTGGAGCGCGGCACATCTCCCGCGGCATCCCGGTC 180
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Db 435 ATGTTGTGATATCCGATACCAAGATGAAGACAGCAGCAACCAATTACATATTAAAC 494
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Db 555 ATGAATTCCTGGCCCTTTGGGGATGCTGTCGCAAGATAGTAATTTCCATTGATTACTAC 614
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LOCUS Sequence 5 from patent US 6518480.
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ACCESSION AR281681.1 GI:29717436
VERSION AR281681.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1275)
AUTHORS Conklin, B.R.
TITLE Selective target cell activation by expression of a G
protein-coupled receptor activated superiorly by synthetic ligand
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JOURNAL Patent: US 6518480-A 5 11-FEB-2003;

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Best Local Similarity 93.0%; Pred. No. 1.6e-173;  
Matches 1061; Conservative 0; Mismatches 71; Indels 9; Gaps 1;

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Db 1244 G 1244
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Searched: 4390206 seqs, 2959870667 residues

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 6: geneseqn2002as.\*
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- 11: geneseqn2003ds.\*
- 12: geneseqn2004as.\*
- 13: geneseqn2004bs.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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5	1150.8	99.7	1154	12	ADN30508 Human kap
6	1150.8	99.7	1154	12	ADN30507 Human kap
7	1150.8	99.7	1154	12	ADN30511 Human kap
8	1150.8	99.7	1154	12	ADN30509 Human kap
9	1144.4	99.2	1182	8	ABZ42678 Human opi
10	1144.4	99.2	1182	10	AAD58490 Human kap
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12	1144.4	99.2	1182	10	ACA58819 Human sig
13	1144.4	99.2	1182	12	ADN56615 Human pol
14	1141.4	98.9	1143	2	AAT90998 Human kap
15	1140.4	98.8	1142	2	AAT12550 Human kap
16	1136.2	98.5	1284	2	AAT90999 Human kap
17	1136.2	98.5	1284	11	ADL90106 cDNA enco
18	1133.4	98.2	1143	12	ADO30011 Human GPC
19	1130.2	97.9	1143	5	ABI98011 Non-endog
20	999.4	86.6	1275	2	AAT92601 Human kap

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24	963.4	83.5	1875	11	ADL90118	Adl90118 Human kap
25	909.2	78.8	1408	2	AAV49254	AAV49254 Mouse kap
26	909.2	78.8	1410	2	AAQ75926	AAQ75926 Mouse kap
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43	434.6	37.7	1464	10	ADG42250	ADG42250 Mu-Oploid
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#### ALIGNMENTS

##### RESULT 1

ADN30506

ID ADN30506 standard; cDNA; 1154 BP.

XX ADN30506;

AC ADN30506;

XX 12-AUG-2004 (first entry)

DT Human kappa opioid receptor, hKOR, C852T allele.

DE Human; kappa opioid receptor; hKOR; ss; gene; SNP;

XX single nucleotide polymorphism; endogenous opioid system; nociception;

KW neurotransmitter release; learning; memory; cognition; pain; cocaine;

KW amphetamine; alcohol; tobacco; opiate; withdrawal;

KW neuroendocrine function; reproductive function; prolactin regulation;

KW stress responsivity; mood; affect; immune function;

KW gastrointestinal function; analgesia; addictive disease;

KW chromosome 8q11.2.

XX Homo sapiens.

OS Homo sapiens.

XX Key Location/Qualifiers

FT replace(852,C)

FT /\*tag= a

FT /standard\_name= "Single nucleotide polymorphism"

US2004097704-A1.

PD 20-MAY-2004.

XX 13-JUL-2001; 2001US-00904584.

XX 14-JUL-2000; 2000US-0218300P.

XX (KREEK) KREEK M J.

XX (YUFE) YUFEROV V.

XX (LAFO) LAFORGE K S.

XX Kreek MJ, Yufarov V, Laforge KS;

XX WPI; 2004-389204/36.

XX Novel isolated variant allele of human kappa opioid receptor gene, useful

PT

for determining susceptibility in subject to physiological response, condition or disease related to endogenous opioid system.

Example; SEQ ID NO 2; 29pp; English.

The invention relates to an isolated variant allele of a human kappa opioid receptor gene, comprising a DNA sequence having at least one variation in a fully defined wild-type allele of human kappa opioid receptor (hKOR) sequence appearing as ADN30505, where the variation comprises C852T, C948T, C1008T or their combinations. Also included are an isolated nucleic acid molecule selectively hybridizing to the variant, a cloning vector comprising the variant and an origin of replication, an expression vector comprising the variant associated with a promoter, a unicellular host transformed/transfected with the vector and a commercial test kit for determining the presence of at least one variation in a hKOR gene of an allele in a bodily sample taken from a subject. The hKOR variant allele is useful for determining a susceptibility in a subject to at least one physiological response, condition or disease related to the endogenous opioid system, nociception, neurotransmitter release, endogenous opioid system, learning, memory, cognition, pain, cocaine, amphetamine and other stimulants self-administration, behavioural sensitisation to cocaine, opiates, alcohol and tobacco, opiate, amphetamine and alcohol withdrawal, physical dependence and tolerance; neuroendocrine function, reproductive function, prolactin regulation, stress responsiveness, physiology and pathology of mood and affect, immune function, gastrointestinal function. The hKOR variant allele is useful for determining a susceptibility to pain in a subject and is useful for determining a therapeutically effective amount of pain reliever to administer to a subject in order to induce analgesia in the subject. The hKOR variant allele is useful for determining a therapeutically effective amount of therapeutic agent to administer to a subject suffering from at least one addictive disease to treat the at least one addictive disease. The gene for hKOR is located on chromosome 8q11.2. The present sequence is the C852T allele of hKOR.

Sequence 1154 BP; 239 A; 338 C; 287 G; 290 T; 0 U; 0 Other;

Query Match 100.0%; Score 1154; DB 12; Length 1154;  
 Best Local Similarity 100.0%; Pred No. 2.7e-274;  
 Matches 1154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGACTCCCGATCCAGATCTTCCGCGGGAGCGGGCCCTACTCGCGCCCGAGCGCC 60  
 1 ATGACTCCCGATCCAGATCTTCCGCGGGAGCGGGCCCTACTCGCGCCCGAGCGCC 60  
 61 TGCTGCCCCCAACAGCAGCGCTGGTTTCCGCGCTGGCGCCGAGCCCGACAGCGC 120  
 61 TGCTGCCCCCAACAGCAGCGCTGGTTTCCGCGCTGGCGCCGAGCCCGACAGCGC 120  
 121 AGCGCGGCTCGGAGGACGCGAGCTGGAGCCGCGCACATCTCCCGGCCATCCCGGTC 180  
 121 AGCGCGGCTCGGAGGACGCGAGCTGGAGCCGCGCACATCTCCCGGCCATCCCGGTC 180  
 181 ATCATCAGCGGGTCTACTCCGTAGTGTTCGTGGGGTGGTGGGCAACTCGCTGGTC 240  
 181 ATCATCAGCGGGTCTACTCCGTAGTGTTCGTGGGGTGGTGGGCAACTCGCTGGTC 240  
 241 ATGTTCTGTATCATCCCATACACAAAGATGAAGACAGCAACCAATTTACATATTAC 300  
 241 ATGTTCTGTATCATCCCATACACAAAGATGAAGACAGCAACCAATTTACATATTAC 300  
 301 CTGGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCGCTTTTCAGAGTACGGTCTACTTG 360  
 301 CTGGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCGCTTTTCAGAGTACGGTCTACTTG 360  
 361 ATGAATTCCTGGCCCTTTTGGGATGTGCTGTGCAAGATAGTAATTCATTTGATTAATAC 420  
 361 ATGAATTCCTGGCCCTTTTGGGATGTGCTGTGCAAGATAGTAATTCATTTGATTAATAC 420  
 421 AACATGTTCCACGACATCTTCCCTTACCATGATGAGCGTGGACCGCATATTGCCGTG 480  
 421 AACATGTTCCACGACATCTTCCCTTACCATGATGAGCGTGGACCGCATATTGCCGTG 480

QY	481	TGCCACCCCGTGAGAGGCTTTGGACTTCGCGACACCCCTTGAAGGCAAGATCATCAATATC	540
DB	481	TGCCACCCCGTGAGAGGCTTTGGACTTCGCGACACCCCTTGAAGGCAAGATCATCAATATC	540
QY	541	TGCATCTGGCTGCTGTCATCTGTCATCTCTGCAATAGTCTCTTGGAGGCAACAA	600
DB	541	TGCATCTGGCTGCTGTCATCTGTCATCTCTGCAATAGTCTCTTGGAGGCAACAA	600
QY	601	GTCCAGGAGAGGCTCGATGTCATTCAGTGTCTCTTGCAGTTCCTCCAGATGATGACTACTCC	660
DB	601	GTCCAGGAGAGGCTCGATGTCATTCAGTGTCTCTTGCAGTTCCTCCAGATGATGACTACTCC	660
QY	661	TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCTTCGTGATCCCTGCTC	720
DB	661	TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCTTCGTGATCCCTGCTC	720
QY	721	ATCATCATGCTGCTGTACACCTGATGATCTGCTCTCAAGAGGCTCGGCTCTCTTTCT	780
DB	721	ATCATCATGCTGCTGTACACCTGATGATCTGCTCTCAAGAGGCTCGGCTCTCTTTCT	780
QY	781	GGCTCCCGAGAGAAAGATCGCAACCTGCTAGGATCACAGACTGGTCTCTGGTGGTG	840
DB	781	GGCTCCCGAGAGAAAGATCGCAACCTGCTAGGATCACAGACTGGTCTCTGGTGGTG	840
QY	841	GCAGTCTTGGTGTCTGCTGGACTCCCATTCACATATTTCATCTCTGGTGGAGCTCTGGGG	900
DB	841	GCAGTCTTGGTGTCTGCTGGACTCCCATTCACATATTTCATCTCTGGTGGAGCTCTGGGG	900
QY	901	AGACCTCCACAGACAGCTGCTCTCTCCAGTATTACTTTCGATCGCCCTTAGGCTAT	960
DB	901	AGACCTCCACAGACAGCTGCTCTCTCCAGTATTACTTTCGATCGCCCTTAGGCTAT	960
QY	961	ACCAACAGTAGCTGAATCCCAATCTCTACGCGCTTCTTGTGATCAAACTTCAAGCGGTG	1020
DB	961	ACCAACAGTAGCTGAATCCCAATCTCTACGCGCTTCTTGTGATCAAACTTCAAGCGGTG	1020
QY	1021	TTCCGGGACTTCTGCTTCCACTGAAGATGAGGATGGAGCGGCGAGACTAGCAGAGTC	1080
DB	1021	TTCCGGGACTTCTGCTTCCACTGAAGATGAGGATGGAGCGGCGAGACTAGCAGAGTC	1080
QY	1081	CGAATACAGTTCCAGATCTCTTACCTGAGGACATCGATGGGATGAATAAACAGTA	1140
DB	1081	CGAATACAGTTCCAGATCTCTTACCTGAGGACATCGATGGGATGAATAAACAGTA	1140
QY	1141	TGACTAGTCTGGA 1154	
DB	1141	TGACTAGTCTGGA 1154	
RESULT 2			
ADN30505			
ID	ADN30505	standard; cDNA; 1154 BP.	
XX	ADN30505;		
XX	12-AUG-2004	(first entry)	
XX	Human kappa opioid receptor, hKOR, wild-type cDNA.		
XX	Human; kappa opioid receptor; hKOR; ss; gene; SNP;		
KW	single nucleotide polymorphism; endogenous opioid system; nociception;		
KW	neurotransmitter release; learning; memory; cognition; pain; cocaine;		
KW	amphetamine; alcohol; tobacco; opiate; withdrawal;		
KW	neuroendocrine function; reproductive function; prolactin regulation;		
KW	stress responsiveness; mood; affect; immune function;		
KW	gastrointestinal function; analgesia; addictive disease;		
XX	chromosome 8q11.2.		
OS	Homo sapiens.		
XX	Key	Location/Qualifiers	
PH	Variation	replace(36,T)	
FT		/*tag= a	

FT /standard\_name= "Single nucleotide polymorphism"  
 FT replace(843,G)  
 FT /\*tag= b  
 FT /standard\_name= "Single nucleotide polymorphism"  
 FT replace(846,T)  
 FT /\*tag= c  
 FT /standard\_name= "Single nucleotide polymorphism"  
 FT replace(852,T)  
 FT /\*tag= d  
 FT /standard\_name= "Single nucleotide polymorphism"  
 FT replace(948,T)  
 FT /\*tag= e  
 FT /standard\_name= "Single nucleotide polymorphism"  
 FT replace(1008,T)  
 FT /\*tag= f  
 FT /standard\_name= "Single nucleotide polymorphism"

XX US2004097704-A1.

XX 20-MAY-2004.

XX 13-JUL-2001; 2001US-00904584.

XX 14-JUL-2000; 2000US-0218300P.

XX (KREE/) KREEK M J.  
 XX (YUFE/) YUFEROV V.  
 XX (LAPO/) LAFORGE K S.

PI Kreek MJ, Yufarov V, Laforge KS;

XX WPI; 2004-389204/36.

PT Novel isolated variant allele of human kappa opioid receptor gene, useful  
 PT for determining susceptibility in subject to physiological response,  
 PT condition or disease related to endogenous opioid system.

XX Claim 1; SEQ ID NO 1; 29pp; English.

XX The invention relates to an isolated variant allele of a human kappa  
 CC opioid receptor gene, comprising a DNA sequence having at least one  
 CC variation in a fully defined wild-type allele of human kappa opioid  
 CC receptor (hKOR) sequence appearing as ADN30505, where the variation  
 CC comprises C852T, C948T, C1008T or their combinations. Also included are  
 CC an isolated nucleic acid molecule selectively hybridising to the variant,  
 CC a cloning vector comprising the variant and an origin of replication, an  
 CC expression vector comprising the variant associated with a promoter, a  
 CC unicellular host transformed/transfected with the vector and a commercial  
 CC test kit for determining the presence of at least one variation in a hKOR  
 CC gene of an allele in a bodily sample taken from a subject. The hKOR  
 CC variant allele is useful for determining a susceptibility in a subject to  
 CC at least one physiological response, condition or disease related to the  
 CC endogenous opioid system, nociception, neurotransmitter release  
 CC endogenous opioid system, learning, memory, cognition, pain, cocaine,  
 CC amphetamine and other stimulants self-administration, behavioural  
 CC sensitisation to cocaine, opiates, alcohol and tobacco, opiate,  
 CC amphetamine and alcohol withdrawal, physical dependence and tolerance;  
 CC neuroendocrine function, reproductive function, prolactin regulation,  
 CC stress responsivity, physiology and pathology of mood and affect, immune  
 CC function, gastrointestinal function. The hKOR variant allele is useful  
 CC for determining a susceptibility to pain in a subject and is useful for  
 CC determining a therapeutically effective amount of pain reliever to  
 CC administer to a subject in order to induce analgesia in the subject. The  
 CC hKOR variant allele is useful for determining a therapeutically effective  
 CC amount of therapeutic agent to administer to a subject suffering from at  
 CC least one addictive disease to treat the at least one addictive disease.  
 CC The gene for hKOR is located on chromosome 8q11.2. The present sequence  
 CC is the most common, wild-type allele of hKOR.

SQ Sequence 1154 BP; 239 A; 339 C; 287 G; 289 T; 0 U; 0 Other;

Query Match 99.9%; Score 1152.4; DB 12; Length 1154;  
 Best Local Similarity 99.9%; Pred. No. 6.7e-274;

	Matches 1153;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy 1	ATGACTCCCGATCCAGATCTTCCGCGGGAGCCGGCCCTACTCTGCGCCCGAGCGCC	60			
Db 1	ATGACTCCCGATCCAGATCTTCCGCGGGAGCCGGCCCTACTCTGCGCCCGAGCGCC	60			
Qy 61	TGCTGCCCCCACAACAGCAGCGCTGTGTTCCCGCTGGGCGAGCCGACAGCAACGGC	120			
Db 61	TGCTGCCCCCACAACAGCAGCGCTGTGTTCCCGCTGGGCGAGCCGACAGCAACGGC	120			
Qy 121	AGCGCGGCTCGGAGGAGCGCAGCTGAGCGCCGACATCTCCCGGCCATCCCGGTC	180			
Db 121	AGCGCGGCTCGGAGGAGCGCAGCTGAGCGCCGACATCTCCCGGCCATCCCGGTC	180			
Qy 181	ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCTGGGCTTGGTGGGCAACTCGCTGTC	240			
Db 181	ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCTGGGCTTGGTGGGCAACTCGCTGTC	240			
Qy 241	ATGTTCTGTATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTATTTAAC	300			
Db 241	ATGTTCTGTATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTATTTAAC	300			
Qy 301	CTGGCTTTGGCAGATGCTTTAGTTACTACCAACATGCTTTCAGAGTACGGTCTACTTG	360			
Db 301	CTGGCTTTGGCAGATGCTTTAGTTACTACCAACATGCTTTCAGAGTACGGTCTACTTG	360			
Qy 361	ATGAATTCCTGGCCTTTTGGGATGTGCTGTCAAGATAGTAATTTTCATTGATTACTAC	420			
Db 361	ATGAATTCCTGGCCTTTTGGGATGTGCTGTCAAGATAGTAATTTTCATTGATTACTAC	420			
Qy 421	AACATGTTACACGATCTTTCACTTCAACATGATGAGCGTGGACCCCTACATTTCCGCTG	480			
Db 421	AACATGTTACACGATCTTTCACTTCAACATGATGAGCGTGGACCCCTACATTTCCGCTG	480			
Qy 481	TGCCACCCCTGAGGCTTTGGACTTCCGACACACCTTGAAGCAAAAGATCATCAATATC	540			
Db 481	TGCCACCCCTGAGGCTTTGGACTTCCGACACACCTTGAAGCAAAAGATCATCAATATC	540			
Qy 541	TGATCTGGCTGTCTGTCTCATCTGTTGGATCTCTGCAATAGTCTTGGAGGACCAAA	600			
Db 541	TGATCTGGCTGTCTGTCTCATCTGTTGGATCTCTGCAATAGTCTTGGAGGACCAAA	600			
Qy 601	GTCAAGGAAGACGTCGATGTCATTTAGTGTCTTCCAGTTCGAGATGATGACTACTCC	660			
Db 601	GTCAAGGAAGACGTCGATGTCATTTAGTGTCTTCCAGTTCGAGATGATGACTACTCC	660			
Qy 661	TGTTGGACCTCTTCATGAAGATCTGCTTTCATCTTTCGCTTCGATCCCTGCTCTC	720			
Db 661	TGTTGGACCTCTTCATGAAGATCTGCTTTCATCTTTCGCTTCGATCCCTGCTCTC	720			
Qy 721	ATCATCATCTCTGCTACACCTTGATGATCTCTGGTCTCAAGACGCTCCGCTCTTCT	780			
Db 721	ATCATCATCTCTGCTACACCTTGATGATCTCTGGTCTCAAGACGCTCCGCTCTTCT	780			
Qy 781	GGCTCCCGAGAAAGATGCCAACCTCGTAGGATCACAGACTGGTCTCTGGTGGTGGT	840			
Db 781	GGCTCCCGAGAAAGATGCCAACCTCGTAGGATCACAGACTGGTCTCTGGTGGTGGT	840			
Qy 841	GCAGTCTTCTGCTGCTGCTCCATTCACATATTTATTCCTGGTGGAGGCTCTGGGG	900			
Db 841	GCAGTCTTCTGCTGCTGCTCCATTCACATATTTATTCCTGGTGGAGGCTCTGGGG	900			
Qy 901	AGACCTCCACAGCAGCTGCTCTCCAGCTATTACTTCTGCATCGCTCTAGGCTAT	960			
Db 901	AGACCTCCACAGCAGCTGCTCTCCAGCTATTACTTCTGCATCGCTCTAGGCTAT	960			
Qy 961	ACCAACAGTAGCTGAATCCCATTTCTCTACGCTTTTCTTGATGAAACTTCAAGCGGT	1020			
Db 961	ACCAACAGTAGCTGAATCCCATTTCTCTACGCTTTTCTTGATGAAACTTCAAGCGGT	1020			
Qy 1021	TTCCGGGACTTCTGCTTTTCCACTGAAGATGAGGATGGAGCGGCGAGACTAGCAGATC	1080			
Db 1021	TTCCGGGACTTCTGCTTTTCCACTGAAGATGAGGATGGAGCGGCGAGACTAGCAGATC	1080			

QY 1081 CGAAATACAGTTTCAGGATCCTGTTACTGAGGAGACATCGATGGGATGAATAAACAGTA 1140  
DB 1081 CGAAATACAGTTTCAGGATCCTGTTACTGAGGAGACATCGATGGGATGAATAAACAGTA 1140  
QY 1141 TGAAGTACGTTGGA 1154  
DB 1141 TGAAGTACGTTGGA 1154

RESULT 3  
ADRA44858  
ID ADRA44858 standard; cDNA; 1154 BP.  
XX ADRA44858;  
AC  
XX  
DT 18-NOV-2004 (first entry)  
XX Human kappa opioid receptor encoding cDNA SEQ ID NO:30.  
DE  
XX opioid receptor; nerve cell; analgesic; gene therapy; pain; human;  
KW kappa opioid receptor; chromosome 8; gene; ss.  
XX  
OS Homo sapiens.

Key Location/Qualifiers  
CDS 1..1143  
FT /tag= a  
FT /product= "kappa opioid receptor"  
XX  
PN WO2004073646-A2.  
XX  
XX 02-SEP-2004.  
XX 19-FEB-2004; 2004WO-US004914.  
XX 19-FEB-2003; 2003US-0448663P.  
XX (UVRP ) UNIV ROCHESTER.  
XX  
XX Kyrkanides S, Tallents RH;  
XX  
XX WPI: 2004-635472/61.  
DR P-PSDB; ADRA44857.  
DR GENBANK; U17298.

XX New vector for delivering an opioid receptor to a nerve cell comprising a  
PT sequence encoding a mu-opioid receptor and a vector backbone, useful in  
PT preparing a composition for reducing pain.  
PS Disclosure; SEQ ID NO 30; 147pp; English.  
XX  
XX The present invention describes a vector for delivering an opioid  
CC receptor to a nerve cell. The method comprises a sequence encoding an  
CC opioid receptor and a vector backbone. Also described: (1) a cell  
CC comprising the vector or its integrated product; (2) an animal comprising  
CC the cell; (3) reducing pain in a subject; (4) producing the vector; (5)  
CC producing the cell; and (6) an animal produced by the process of  
CC administering the vector to the animal. The vector has analgesic  
CC activity, and can be used in gene therapy. The vector is useful in  
CC preparing a composition for reducing pain in a subject. The present  
CC sequence encodes the human kappa opioid receptor, which is used in the  
CC exemplification of the present invention. The human kappa opioid receptor  
CC gene is located on chromosome 8, more specifically to 8q11-12.  
XX  
XX Sequence 1154 BP; 239 A; 339 C; 287 G; 289 T; 0 U; 0 Other;  
SQ  
Query Match 99.9%; Score 1152.4; DB 13; Length 1154;  
Best Local Similarity 99.9%; Pred. No. 6.7e-274;  
Matches 1153; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 ATGACTCCCGATCCAGATCTTCGCGGGAGCGGGCCCTACTCGGCCCGAGCGCC 60  
|||||

DB 1 ATGACTCCCGATCCAGATCTTCGCGGGAGCGGGCCCTACTCGGCCCGAGCGCC 60  
QY 61 TGCCTGCCCGCCCAACAGAGCGCTGTTTCCCGGCTGGGCGGAGCCGACAGCAAGCGC 120  
DB 61 TGCCTGCCCGCCCAACAGAGCGCTGTTTCCCGGCTGGGCGGAGCCGACAGCAAGCGC 120  
QY 121 AGCGCGGCTCGGAGGAGCGCGACGTGGAGGCCCGCGACATCTCCCGGCCATCCCGGTC 180  
DB 121 AGCGCGGCTCGGAGGAGCGCGACGTGGAGGCCCGCGACATCTCCCGGCCATCCCGGTC 180  
QY 181 ATCATCACGCGGCTTACTCCGTAGTGTTCGTGGGCTTGGTGGGCAATCGTGGTC 240  
DB 181 ATCATCACGCGGCTTACTCCGTAGTGTTCGTGGGCTTGGTGGGCAATCGTGGTC 240  
QY 241 ATGTTCTGTGATCATCCGATACACAAGATGAAGACAGCAACCAATTTACATATTAAC 300  
DB 241 ATGTTCTGTGATCATCCGATACACAAGATGAAGACAGCAACCAATTTACATATTAAC 300  
QY 301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCTTTCAGAGTACGGTCTACTTG 360  
DB 301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCTTTCAGAGTACGGTCTACTTG 360  
QY 361 ATGAATTCCTGGCCTTTTGGGATGTGCTGTGCAAGTAGTAATTTCCATTGATTACTAC 420  
DB 361 ATGAATTCCTGGCCTTTTGGGATGTGCTGTGCAAGTAGTAATTTCCATTGATTACTAC 420  
QY 421 AACATGTTTACACAGCATCTTCACCTTGACATGATGAGCGTGGACCGGTACATTGCCGTG 480  
DB 421 AACATGTTTACACAGCATCTTCACCTTGACATGATGAGCGTGGACCGGTACATTGCCGTG 480  
QY 481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCAACCCCTTGAAGGCAAGATCATCAATATC 540  
DB 481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCAACCCCTTGAAGGCAAGATCATCAATATC 540  
QY 541 TGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
DB 541 TGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
QY 601 GTGAGGAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
DB 601 GTGAGGAGAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
QY 661 TGGTGGGACCTTTCATGAAGATCTGCGCTTTCATCTTTCGCTGCTGCTGCTGCTGCTGCT 720  
DB 661 TGGTGGGACCTTTCATGAAGATCTGCGCTTTCATCTTTCGCTGCTGCTGCTGCTGCTGCT 720  
QY 721 ATCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
DB 721 ATCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
QY 781 GGCTCCCGAGAGAGATCGCAACCTGCTAGGATCACAGACTGCTGCTGCTGCTGCTGCTGCTG 840  
DB 781 GGCTCCCGAGAGAGATCGCAACCTGCTAGGATCACAGACTGCTGCTGCTGCTGCTGCTGCTG 840  
QY 841 GGAGTCTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
DB 841 GGAGTCTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
QY 901 AGCACCTCCACAGACACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
DB 901 AGCACCTCCACAGACACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
QY 961 ACCAACAGTAGCTGAATCCCAATTCCTACGCGCTTCTTGTGATGAATACTCAAGCGGTGT 1020  
DB 961 ACCAACAGTAGCTGAATCCCAATTCCTACGCGCTTCTTGTGATGAATACTCAAGCGGTGT 1020  
QY 1021 TTCCGGGACTTCTGCTTTCCTGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 1080  
DB 1021 TTCCGGGACTTCTGCTTTCCTGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 1080  
QY 1081 CGAAATACAGTTTCAGGATCCTGTTACTGAGGAGACATCGATGGGATGAATAAACAGTA 1140  
DB 1081 CGAAATACAGTTTCAGGATCCTGTTACTGAGGAGACATCGATGGGATGAATAAACAGTA 1140



QY 1141 TGACTAGTCGTGGA 1154  
 XX |||||||  
 Db 1141 TGACTAGTCGTGGA 1154

RESULT 4  
 ADN30510  
 ID ADN30510 standard; cDNA; 1154 BP.  
 XX  
 AC ADN30510;  
 XX  
 DT 12-AUG-2004 (first entry)  
 DE Human kappa opioid receptor, hKOR, A843G allele.  
 XX  
 KW Human; kappa opioid receptor; hKOR; ss; gene; SNP;  
 KW single nucleotide polymorphism; endogenous opioid system; nociception;  
 KW neurotransmitter release; learning; memory; cognition; pain; cocaine;  
 KW amphetamine; alcohol; tobacco; opiate; withdrawal;  
 KW neuroendocrine function; reproductive function; prolactin regulation;  
 KW stress responsiveness; mood; affect; immune function;  
 KW gastrointestinal function; analgesia; addictive disease;  
 KW chromosome 8q11.2.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT allele replace(843,A)  
 FT /\*tag= a  
 FT /standard\_name= "single nucleotide polymorphism"  
 XX  
 PN US2004097704-A1.  
 XX  
 PD 20-MAY-2004.  
 XX  
 PF 13-JUL-2001; 2001US-00904584.  
 XX  
 PR 14-JUL-2000; 2000US-0218300P.  
 XX  
 PA (KREE/) KREEK M J.  
 PA (YUFE/) YUFEROV V.  
 PA (LAFO/) LAFORGE K S.  
 XX  
 PI Kreek MJ, Yufarov V, Laforge KS;  
 XX  
 DR WPI; 2004-389204/36.  
 XX  
 PT Novel isolated variant allele of human kappa opioid receptor gene, useful  
 PT for determining susceptibility in subject to physiological response,  
 PT condition or disease related to endogenous opioid system.  
 XX  
 PS Example; SEQ ID NO 6; 29pp; English.  
 XX

The invention relates to an isolated variant allele of a human kappa  
 CC opioid receptor gene, comprising a DNA sequence having at least one  
 CC variation in a fully defined wild-type allele of human kappa opioid  
 CC receptor (hKOR) sequence appearing as ADN30505, where the variation  
 CC comprises C852T, C948T, C1008T or their combinations. Also included are  
 CC an isolated nucleic acid molecule selectively hybridising to the variant,  
 CC a cloning vector comprising the variant and an origin of replication, an  
 CC expression vector comprising the variant associated with a promoter, a  
 CC unicellular host transformed/transfected with the vector and a commercial  
 CC test kit for determining the presence of at least one variation in a hKOR  
 CC gene of an allele in a bodily sample taken from a subject. The hKOR  
 CC variant allele is useful for determining a susceptibility in a subject to  
 CC at least one physiological response, condition or disease related to the  
 CC endogenous opioid system, nociception, neurotransmitter release  
 CC endogenous opioid system, learning, memory, cognition, pain, cocaine,  
 CC amphetamine and other stimulants self-administration, behavioural  
 CC sensitisation to cocaine, opiates, alcohol and tobacco, opiate,  
 CC amphetamine and alcohol withdrawal, physical dependence and tolerance;  
 CC neuroendocrine function, reproductive function, prolactin regulation,

CC stress responsiveness, physiology and pathology of mood and affect, immune  
 CC function, gastrointestinal function. The hKOR variant allele is useful  
 CC for determining a susceptibility to pain in a subject and is useful for  
 CC determining a therapeutically effective amount of pain reliever to  
 CC administer to a subject in order to induce analgesia in the subject. The  
 CC hKOR variant allele is useful for determining a therapeutically effective  
 CC amount of therapeutic agent to administer to a subject suffering from at  
 CC least one addictive disease to treat the at least one addictive disease.  
 CC The gene for hKOR is located on chromosome 8q11.2. The present sequence  
 CC is the A843G allele of hKOR.  
 XX  
 SQ Sequence 1154 BP; 238 A; 339 C; 288 G; 289 T; 0 U; 0 Other;  
 XX

Query Match 99.7%; Score 1150.8; DB 12; Length 1154;  
 Best Local Similarity 99.8%; Pred. No. 1.7e-273;  
 Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGACTCCCGATCCAGATCTTCGCGGGAGCGGGCCCTACTGCGCCCGAGCGCC 60  
 Db |||||||  
 QY 1 ATGACTCCCGATCCAGATCTTCGCGGGAGCGGGCCCTACTGCGCCCGAGCGCC 60  
 Db |||||||  
 QY 61 TGCCTGCCCGCCCAACAGCAGCGCTGCTTCCCGGCTGGGCGGAGCGGAGCAACGGC 120  
 Db |||||||  
 QY 61 TGCCTGCCCGCCCAACAGCAGCGCTGCTTCCCGGCTGGGCGGAGCGGAGCAACGGC 120  
 Db |||||||  
 QY 121 AGCGCCGGCTCGGAGGACGGCGAGCTGGAGCGCGGCACATCTCCCGGCCCATCCGGTC 180  
 Db |||||||  
 QY 121 AGCGCCGGCTCGGAGGACGGCGAGCTGGAGCGCGGCACATCTCCCGGCCCATCCGGTC 180  
 Db |||||||  
 QY 181 ATCATCAAGCGGCTCTACTCCGTAGTGTTCGTGCGGCTGGGCGGAGCACTCGCTGTC 240  
 Db |||||||  
 QY 181 ATCATCAAGCGGCTCTACTCCGTAGTGTTCGTGCGGCTGGGCGGAGCACTCGCTGTC 240  
 Db |||||||  
 QY 241 ATGTTCTGTATCATCCGATACACAAAGATGAGGACGACCAACCATTTACATTTTAAAC 300  
 Db |||||||  
 QY 241 ATGTTCTGTATCATCCGATACACAAAGATGAGGACGACCAACCATTTACATTTTAAAC 300  
 Db |||||||  
 QY 301 CTGGCTTTGGCAGATGCTTTAGTTACTCAACCATGCGCTTTTCAGAGTACGGTCTACTTG 360  
 Db |||||||  
 QY 301 CTGGCTTTGGCAGATGCTTTAGTTACTCAACCATGCGCTTTTCAGAGTACGGTCTACTTG 360  
 Db |||||||  
 QY 361 ATGAATTCCTGGGCTTTTGGGATGTCTGTGCAAGATAGTAAATTTCCATTGATTACTAC 420  
 Db |||||||  
 QY 361 ATGAATTCCTGGGCTTTTGGGATGTCTGTGCAAGATAGTAAATTTCCATTGATTACTAC 420  
 Db |||||||  
 QY 421 AACATGTTCCACGACATCTTCACTTGACCATGATGAGCGTGGACCGGTATGCGGTG 480  
 Db |||||||  
 QY 421 AACATGTTCCACGACATCTTCACTTGACCATGATGAGCGTGGACCGGTATGCGGTG 480  
 Db |||||||  
 QY 481 TGCCACCCCGTGAAGGCTTTGGGACTCCGACACCCCTTGAAGGCAAGATCATCAATATC 540  
 Db |||||||  
 QY 481 TGCCACCCCGTGAAGGCTTTGGGACTCCGACACCCCTTGAAGGCAAGATCATCAATATC 540  
 Db |||||||  
 QY 541 TGCAATCTGGCTGTCTGTCATCTGTTGGCATCTGCAATAGTCTTGGAGGACCAAA 600  
 Db |||||||  
 QY 541 TGCAATCTGGCTGTCTGTCATCTGTTGGCATCTGCAATAGTCTTGGAGGACCAAA 600  
 Db |||||||  
 QY 601 GTACGGGAACAGTCGATGTCATGTCCTTGGAGTCCGAGTCCGAGATGATGACTACTCC 660  
 Db |||||||  
 QY 601 GTACGGGAACAGTCGATGTCATGTCCTTGGAGTCCGAGTCCGAGATGATGACTACTCC 660  
 Db |||||||  
 QY 661 TGGTGGGACCTCTTTCATGAAGATCTGGCTCTTCAATCTTTCGCTTCGATGCTCTCTC 720  
 Db |||||||  
 QY 661 TGGTGGGACCTCTTTCATGAAGATCTGGCTCTTCAATCTTTCGCTTCGATGCTCTCTC 720  
 Db |||||||  
 QY 721 ATCATCATCTGCTGCTACACCCCTGATGATCTCGGTCTCAAGAGCGTCCGGCTCTTTCT 780  
 Db |||||||  
 QY 721 ATCATCATCTGCTGCTACACCCCTGATGATCTCGGTCTCAAGAGCGTCCGGCTCTTTCT 780  
 Db |||||||  
 QY 781 GGCTCCCGAGAGAAAGATCCCAACCTCGGTAGGATCACAGACTGGTCTGGTGGTGGTG 840  
 Db |||||||  
 QY 781 GGCTCCCGAGAGAAAGATCCCAACCTCGGTAGGATCACAGACTGGTCTGGTGGTGGTG 840  
 Db |||||||



Db	541		TGCATCTGGCTGCTGTGTCATCTGTTGGCATCTCTGCATAGTTCCTTGGAGGCCACAAA	600
Qy	601		GTCAAGGAAGACGTCGATGTCATTTAGTGTCTTGTGAGTTCCTGCAGTATGACTACTCTCC	660
Db	601		GTCAAGGAAGACGTCGATGTCATTTAGTGTCTTGTGAGTTCCTGCAGTATGACTACTCTCC	660
Qy	661		TGTTGGGACCTCTTTCAATGAAGATCTGGTCTTTCACTTTGCCTTCGTGATCCCTGTCTTC	720
Db	661		TGTTGGGACCTCTTTCAATGAAGATCTGGTCTTTCACTTTGCCTTCGTGATCCCTGTCTTC	720
Qy	721		ATCATCATGCTCTGCTACCTCATGATCTCTGCGTCTCAAGACGCTCCGCTCTCTTTTCT	780
Db	721		ATCATCATGCTCTGCTACCTCATGATCTCTGCGTCTCAAGACGCTCCGCTCTCTTTTCT	780
Qy	781		GGCTCCCGAGAGAAGATCGCAACCTGGGTAGGATCACAGACTGGTCTCTGGTGGTGGTG	840
Db	781		GGCTCCCGAGAGAAGATCGCAACCTGGGTAGGATCACAGACTGGTCTCTGGTGGTGGTG	840
Qy	841		GCAGCTCTTCTGTTCTGCTGGACTCCCATTCACATATTTTCATCTTGGTGGAGGCTCTCGGG	900
Db	841		GCAGCTCTTCTGTTCTGCTGGACTCCCATTCACATATTTTCATCTTGGTGGAGGCTCTCGGG	900
Qy	901		AGCACTCCCAACAGACAGCTGCTCTCTCAGCTATTACTTCTGCATCGCCTTAGGCTAT	960
Db	901		AGCACTCCCAACAGACAGCTGCTCTCTCAGCTATTACTTCTGCATCGCCTTAGGCTAT	960
Qy	961		ACCAACAGTAGCCTGAATCCCATTTCTTACGCCCTTTCTTGATGAAACTTTCAAGCGGTGT	1020
Db	961		ACCAACAGTAGCCTGAATCCCATTTCTTACGCCCTTTCTTGATGAAACTTTCAAGCGGTGT	1020
Qy	1021		TTCCGGGACTTCTGCTTTTCCACTGAAGATGAGGATGGAGCGGCAGAGCACTTAGCAGAGTC	1080
Db	1021		TTCCGGGACTTCTGCTTTTCCACTGAAGATGAGGATGGAGCGGCAGAGCACTTAGCAGAGTC	1080
Qy	1081		CGAAATACAGTTACAGGATCCTGCTTACTCTGAGGACATCGATGGATGTAATAACACAGTA	1140
Db	1081		CGAAATACAGTTACAGGATCCTGCTTACTCTGAGGACATCGATGGATGTAATAACACAGTA	1140
Qy	1141		TGACTAGTCGTGGA	1154
Db	1141		TGACTAGTCGTGGA	1154

RESULT 6  
ADN30507  
ID ADN30507 standard; cDNA; 1154 BP.

AC ADN30507;

12-AUG-2004 (first entry)

DE Human kappa opioid receptor, hKOR, C948T allele. XX

Human; kappa opioid receptor; hKOR; ss; gene; SNP;  
single nucleotide polymorphism; endogenous opioid system; nociception;  
neurotransmitter release; learning; memory; cognition; pain; cocaine;  
amphetamines; alcohol; tobacco; opiate; withdrawal;  
neuroendocrine function; reproductive function; prolactin regulation;  
stress responsivity; mood; affect; immune function;  
gastrointestinal function; analgesia; additive disease;  
chromosome 8q11.2

OS Homo sapiens.

Accession	Key	Location/Qualifiers
FH	allele	replace(948,C)
FT		

```

FI /- tag= a
FT /standard name= "Single nucleotide polymorphism"

```

AA  
PN  
US2004097704-A1.

20-MAY-2004.

XX	13-JUL-2001; 2001US-00904584.	
PF		
XX	14-JUL-2000; 2000US-0218300P.	
PR		
XX	(KREE/) KREEK M J.	
XX	(YUFE/) YUFEROV V.	
PA	(LAFO/) LAFORGE K S.	
PA		
XX	Kreek MJ, Yufarov V, Laforge KS;	
PI		
XX		
XX	WPI; 2004-389204/35.	
DR		
XX		
XX	Novel isolated variant allele of human kappa opioid receptor gene, useful	
PT	for determining susceptibility in subject to physiological response,	
PT	condition or disease related to endogenous opioid system.	
PT		
XX	Example; SEQ ID NO 3; 290p; English.	
XX		
PS		

The invention relates to an isolated variant allele of a human kappa opioid receptor gene, comprising a DNA sequence having at least one variation in a fully defined wild-type allele of human kappa opioid receptor (hKOR) sequence appearing as ADN30505, where the variation comprises C952r, C948r, C1008r or their combinations. Also included are an isolated nucleic acid molecule selectively hybridising to the variant, a cloning vector comprising the variant and an origin of replication, an expression vector comprising the variant associated with a promoter, a unicellular host transformed/transfected with the vector and a commercial test kit for determining the presence of at least one variation in a hKOR gene of an allele in a bodily sample taken from a subject. The hKOR variant allele is useful for determining a susceptibility in a subject to at least one physiological response, condition or disease related to the endogenous opioid system, nociception, neurotransmitter release endogenous opioid system, learning, memory, cognition, pain, cocaine, amphetamine and other stimulants self-administration, behavioural sensitisation to cocaine, opiates, alcohol and tobacco, opiate, amphetamine and alcohol withdrawal, physical dependence and tolerance; neuroendocrine function, reproductive function, prolactin regulation, stress reactivity, physiology and pathology of mood and affect, immune function, gastrointestinal function. The hKOR variant allele is useful for determining a susceptibility to pain in a subject and is useful for determining a therapeutically effective amount of pain reliever to administer to a subject in order to induce analgesia in the subject. The hKOR variant allele is useful for determining a therapeutically effective amount of therapeutic agent to administer to a subject suffering from at least one addictive disease to treat the at least one addictive disease. The gene for hKOR is located on chromosome 8q11.2. The present sequence is the C948r allele of hKOR.

Sequence 1154 BP: 239 A: 338 C: 287 G: 290 T: 0 U: 0 Other: XX

Query Match	99.7%	Score 1150.8;	DB 12;	Length 1154;
Best Local Similarity	99.8%;	Pred. No. 1.7e-273;		
Matches 1152;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	1	ATGGATCCCGGATCAGATCTTCGGGGGAGCGGGCCCTACCTGGGCCCGAGCGCC	60	
Db	1	ATGGATCCCGGATCAGATCTTCGGGGGAGCGGGGCCCTACCTGGGCCCGAGCGCC	60	
Qy	61	TGCGTGTCCCCCAACAGCAGCGCGCTGTGTTTCGGGGCTGGGCGGAGCCGACAGCAAACGGC	120	
Db	61	TGCGTGTCCCCCAACAGCAGCGCGCTGTGTTTCGGGGCTGGGCGGAGCCGACAGCAAACGGC	120	
Qy	121	AGCGCGGGTCGGAGGACGGCGCAGCTGGAGCCCGCGCACATCTCCC CGGGCATCCCCGGTC	180	
Db	121	AGCGCGGGTCGGAGGACGGCGCAGCTGGAGCCCGCGCACATCTCCC CGGGCATCCCCGGTC	180	
Qy	181	ATCATCAACGCGGTCTACTCCGTAGTGTTCGTGTGGGCTTGGTGGGCAACTCGCTGGTC	240	
Db	181	ATCATCAACGCGGTCTACTCCGTAGTGTTCGTGTGGGCTTGGTGGGCAACTCGCTGGTC	240	
Qy	241	ATGTTGTGTGATCATCCGATACACAAAGATCAAGACAGCAACCAACATTTTACATATTTTAAAC	300	

Db 241 ATGTTCTGTCATCCGATACCAAGATGACAGACAGCAACCAACATTTACATATTTAATC 300  
 Qy 301 CTGGCTTTGGCAGATGCTTTAGTACTACAAACATGCTTTTACAGAGTACGGTCTACTTG 360  
 Db 301 CTGGCTTTGGCAGATGCTTTAGTACTACAAACATGCTTTTACAGAGTACGGTCTACTTG 360  
 Qy 361 ATGAATTCCTGGCTTTGGGATGCTGTCGAAGATAGTAAATTCATTCATTAATCTAC 420  
 Db 361 ATGAATTCCTGGCTTTGGGATGCTGTCGAAGATAGTAAATTCATTCATTAATCTAC 420  
 Qy 421 AACATGTTCAACAGCATCTTCACTTTCACCATGATGAGCGTGGACCGCTACATTTGCCGTG 480  
 Db 421 AACATGTTCAACAGCATCTTCACTTTCACCATGATGAGCGTGGACCGCTACATTTGCCGTG 480  
 Qy 481 TGCACCCCGTGAAGCTTTGGATCTTCGACACACCTTGAAGCAAAAGATCATCAATATC 540  
 Db 481 TGCACCCCGTGAAGCTTTGGATCTTCGACACACCTTGAAGCAAAAGATCATCAATATC 540  
 Qy 541 TGCATCTGGCTGCTGCTGTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGCACCAAA 600  
 Db 541 TGCATCTGGCTGCTGCTGTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGCACCAAA 600  
 Qy 601 GTGAGGAAGACCTCGATGTCATTGAGTGTCTCTTCAGTTCCTCAGATTCCTCAGATGATCACTCTCC 660  
 Db 601 GTGAGGAAGACCTCGATGTCATTGAGTGTCTCTTCAGTTCCTCAGATGATGATCACTCTCC 660  
 Qy 661 TGGTGGACCTCTTCAATGAAGATCTGGTCTTCATCTTTTGGCTTCGTGATTCCTGTCCTC 720  
 Db 661 TGGTGGACCTCTTCAATGAAGATCTGGTCTTCATCTTTTGGCTTCGTGATTCCTGTCCTC 720  
 Qy 721 ATCATCATGCTGCTGCTACACCTCGATGATCTCGCTCTCAAGAGCGTCCGGCTCTCTTCT 780  
 Db 721 ATCATCATGCTGCTGCTACACCTCGATGATCTCGCTCTCAAGAGCGTCCGGCTCTCTTCT 780  
 Qy 781 GGCTCCCGAGAGAAAGATCCAACTCGTAGATCACCAGACTGGTCTCTGCTGGTGGTG 840  
 Db 781 GGCTCCCGAGAGAAAGATCCAACTCGTAGATCACCAGACTGGTCTCTGCTGGTGGTG 840  
 Qy 841 GCAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
 Db 841 GCAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
 Qy 901 AGCAGCTTCCACAGCAGCTGCTCTCTCCAGCTATTACTTCTGCTGCTGCTGCTGCTGCT 960  
 Db 901 AGCAGCTTCCACAGCAGCTGCTCTCTCCAGCTATTACTTCTGCTGCTGCTGCTGCTGCT 960  
 Qy 961 ACCAACAGTACCTGATCCCAATCTCTAGCCCTTTCTTGATGAAACCTTCAAGCGGTGT 1020  
 Db 961 ACCAACAGTACCTGATCCCAATCTCTAGCCCTTTCTTGATGAAACCTTCAAGCGGTGT 1020  
 Qy 1021 TTCGGGACTTCTGCTTCCACTGAAAGATGAGTGGAGCGGCGAGAGCACTAGCAGATC 1080  
 Db 1021 TTCGGGACTTCTGCTTCCACTGAAAGATGAGTGGAGCGGCGAGAGCACTAGCAGATC 1080  
 Qy 1081 CGAAATACAGTTCAGGATCTGCTTACTCTGAGGACATCATGGGATGAATAACCAAGTA 1140  
 Db 1081 CGAAATACAGTTCAGGATCTGCTTACTCTGAGGACATCATGGGATGAATAACCAAGTA 1140  
 Qy 1141 TGACTAGTCTGGA 1154  
 Db 1141 TGACTAGTCTGGA 1154

RESULT 7  
 ADN30511  
 ID ADN30511 standard; cDNA; 1154 BP.

AC ADN30511;

XX 12-AUG-2004 (first entry)

XX Human kappa opioid receptor, hKOR, C856T allele.

XX

KW Human; kappa opioid receptor; hKOR; ss; gene; SNP;  
 KW single nucleotide polymorphism; endogenous opioid system; nociception;  
 KW neurotransmitter release; learning; memory; cognition; pain; cocaine;  
 KW amphetamine; alcohol; tobacco; opiate; withdrawal;  
 KW neuroendocrine function; reproductive function; prolactin regulation;  
 KW stress responsivity; mood; affect; immune function;  
 KW gastrointestinal function; analgesia; addictive disease;  
 KW Chromosome 8q11.2.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FT allele replace(846,C)  
 FT /tag= a

XX /standard\_name= "Single nucleotide polymorphism"

XX US2004097704-A1.

XX 20-MAY-2004.

XX 13-JUL-2001; 2001US-00904584.

XX 14-JUL-2000; 2000US-0218300P.

XX (KREE/) KREEK M J.

XX (YUPE/) YUPEROV V.

XX (LAFC/) LAForge K S.

XX Kreek WJ, Yufarov V, Laforge KS;

XX WPI; 2004-389204/36.

XX Novel isolated variant allele of human kappa opioid receptor gene, useful for determining susceptibility in subject to physiological response, condition or disease related to endogenous opioid system.

XX Example; SEQ ID NO 7; 29pp; English.

XX The invention relates to an isolated variant allele of a human kappa  
 CC opioid receptor gene, comprising a DNA sequence having at least one  
 CC variation in a fully defined wild-type allele of human kappa opioid  
 CC receptor (hKOR) sequence appearing as ADN30505, where the variation  
 CC comprises C852T, C948T, C1008T or their combinations. Also included are  
 CC an isolated nucleic acid molecule selectively hybridising to the variant,  
 CC a cloning vector comprising the variant and an origin of replication, an  
 CC expression vector comprising the variant associated with a promoter, a  
 CC unicellular host transfected with the vector and a commercial  
 CC test kit for determining the presence of at least one variation in a hKOR  
 CC gene of an allele in a bodily sample taken from a subject. The hKOR  
 CC variant allele is useful for determining a susceptibility in a subject to  
 CC at least one physiological response, condition or disease related to the  
 CC endogenous opioid system, nociception, neurotransmitter release,  
 CC amphetamine and other stimulants self-administration, behavioural  
 CC sensitisation to cocaine, opiates, alcohol and tobacco, opiate,  
 CC amphetamine and alcohol withdrawal, physical dependence and tolerance;  
 CC neuroendocrine function, reproductive function, prolactin regulation,  
 CC stress responsivity, physiology and pathology of mood and affect, immune  
 CC function, gastrointestinal function. The hKOR variant allele is useful  
 CC for determining a susceptibility to pain in a subject and is useful for  
 CC determining a therapeutically effective amount of pain reliever to  
 CC administer to a subject in order to induce analgesia in the subject. The  
 CC hKOR variant allele is useful for determining a therapeutically effective  
 CC amount of therapeutic agent to administer to a subject suffering from at  
 CC least one addictive disease to treat the at least one addictive disease.  
 CC The gene for hKOR is located on chromosome 8q11.2. The present sequence  
 CC is the C846T allele of hKOR.

XX Sequence 1154 BP; 239 A; 338 C; 287 G; 290 T; 0 U; 0 Other;

XX Query Match 99.7%; Score 1150.8; DB 12; Length 1154;

XX Best Local Similarity 99.8%; Pred. No. 1.7e-273; Indels 0; Gaps 0;

XX Matches 1152; Conservative 0; Mismatches 2;

```
Qy 1 ATGGAATCCCGATCCAGATCTTCCGGGGAGCCGGGCCCTACCTGCGCCCCGAGGGCC 60
Db 1 ATGGAATCCCGATCCAGATCTTCCGGGGAGCCGGGCCCTACCTGCGCCCCGAGGGCC 60
Qy 61 TGCCTGCCCCCAACAGCAGGCGCTTGTTCCTCCGGCTGGGGCCGAGCCGACAGCAACGGC 120
Db 61 TGCCTGCCCCCAACAGCAGGCGCTTGTTCCTCCGGCTGGGGCCGAGCCGACAGCAACGGC 120
Qy 121 AGCCCGGCTCGAGGAGCGCAGCTGGAGCCCGCACATCTCCCGGCCCATCCCGGTC 180
Db 121 AGCCCGGCTCGAGGAGCGCAGCTGGAGCCCGCACATCTCCCGGCCCATCCCGGTC 180
Qy 181 ATCATCAGCGCGGTCTACTCCGTAGTGTTCGTCTGGGCTTGGTGGGCAACTCGCTGGTC 240
Db 181 ATCATCAGCGCGGTCTACTCCGTAGTGTTCGTCTGGGCTTGGTGGGCAACTCGCTGGTC 240
Qy 241 ATGTTCTGTATCATCCGATACACAAAGATGAAGCAGCAACCAACATTTACATATTAAAC 300
Db 241 ATGTTCTGTATCATCCGATACACAAAGATGAAGCAGCAACCAACATTTACATATTAAAC 300
Qy 301 CTGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
Db 301 CTGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
Qy 361 ATGAATTCCTGGCCCTTTTGGGATGTCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
Db 361 ATGAATTCCTGGCCCTTTTGGGATGTCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
Qy 421 AACATGTTCCAGCATCTTCACTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 480
Db 421 AACATGTTCCAGCATCTTCACTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 480
Qy 481 TGCCACCCCGTGAAGGCTTTGAGCTTCGACACCCCTTGAAGGCAAGATCATCAATATC 540
Db 481 TGCCACCCCGTGAAGGCTTTGAGCTTCGACACCCCTTGAAGGCAAGATCATCAATATC 540
Qy 541 TGCAATCTGGTGTCTGTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGCAACAAA 600
Db 541 TGCAATCTGGTGTCTGTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGCAACAAA 600
Qy 601 GTACGGAAGACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
Db 601 GTACGGAAGACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
Qy 661 TGGTGGACCTCTTTCATGAAGATCTGGTCTTTCATCTTTCGCTTTCGCTTTCGCTTTC 720
Db 661 TGGTGGACCTCTTTCATGAAGATCTGGTCTTTCATCTTTCGCTTTCGCTTTCGCTTTC 720
Qy 721 ATCATCATCTGCTGTCTACACCTGATGATGATGATGATGATGATGATGATGATGATGAT 780
Db 721 ATCATCATCTGCTGTCTACACCTGATGATGATGATGATGATGATGATGATGATGATGAT 780
Qy 781 GGCTCCGAGAGAAGATCGAACCTGGTGTAGGATCACAGACTGTGCTGGTGGTGGTG 840
Db 781 GGCTCCGAGAGAAGATCGAACCTGGTGTAGGATCACAGACTGTGCTGGTGGTGGTG 840
Qy 841 GCAGTCTTCTGTGCTGCTGACTCCCAATTCACATATTTTCCTGCTGGAGGCTCTCGGG 900
Db 841 GCAGTCTTCTGTGCTGCTGACTCCCAATTCACATATTTTCCTGCTGGAGGCTCTCGGG 900
Qy 901 AGCACTCTCCACAGCAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCTTACGGCTAT 960
Db 901 AGCACTCTCCACAGCAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCTTACGGCTAT 960
Qy 961 ACCAACAGTAGCTGAATCCCATCTCTACGCCCTTCTTGATGAAAATCTCAAGCGGTGT 1020
Db 961 ACCAACAGTAGCTGAATCCCATCTCTACGCCCTTCTTGATGAAAATCTCAAGCGGTGT 1020
Qy 1021 TTCCGGGACTTCTGCTTTCCACTGAGATGAGGATGGAGCGGACGACCTAGCAGAGTC 1080
Db 1021 TTCCGGGACTTCTGCTTTCCACTGAGATGAGGATGGAGCGGACGACCTAGCAGAGTC 1080
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Qy 1081 CGAAATACAGTTCCAGATCTCTTACCTGAGGACATCGATGGATGAATAAACACAGTA 1140
Db 1081 CGAAATACAGTTCCAGATCTCTTACCTGAGGACATCGATGGATGAATAAACACAGTA 1140
Qy 1141 TGAAGTCTGCTGGA 1154
Db 1141 TGAAGTCTGCTGGA 1154

RESULT 8
ADN30509
ID ADN30509 standard; cDNA; 1154 BP.
XX
AC ADN30509;
XX AC
DT 12-AUG-2004 (first entry)
XX
DE Human kappa opioid receptor, hKOR, G36T allele.
XX
KW Human; kappa opioid receptor; hKOR; ss; gene; SNP;
KW single nucleotide polymorphism; endogenous opioid system; nociception;
KW neurotransmitter release; learning; memory; cognition; pain; cocaine;
KW amphetamine; alcohol; tobacco; opiate; withdrawal;
KW neuroendocrine function; reproductive function; prolactin regulation;
KW stress responsiveness; mood; affect; immune function;
KW gastrointestinal function; analgesia; addictive disease;
KW chromosome 8q11.2.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT allele replace(36,G)
FT FT /*Tag= a
FT FT /standard_name= "Single nucleotide polymorphism"
XX
PN US2004097704-A1.
XX
PD 20-MAY-2004.
XX
PF 13-JUL-2001; 2001US-00904584.
XX
PR 14-JUL-2000; 2000US-0218300P.
XX
XX (KREE/) KREEK M J.
XX (YUFE/) YUFEROV V.
XX (LAFO/) LAFORGE K S.
XX
PI Kreek MJ, Yufarov V, Laforge KS;
XX
XX WPI; 2004-389204/36.
XX
PT Novel isolated variant allele of human kappa opioid receptor gene, useful
PT for determining susceptibility in subject to physiological response,
PT condition or disease related to endogenous opioid system.
XX
PS Example; SEQ ID NO 5; 29pp; English.
XX
XX The invention relates to an isolated variant allele of a human kappa
XX opioid receptor gene, comprising a DNA sequence having at least one
XX variation in a fully defined wild-type allele of human kappa opioid
XX receptor (hKOR) sequence appearing as ADN30509, where the variation
XX comprises C852T, C948T, C1008T or their combinations. Also included are
XX an isolated nucleic acid molecule selectively hybridising to the variant,
XX a cloning vector comprising the variant and an origin of replication, an
XX expression vector comprising the variant associated with a promoter, a
XX unicellular host transformed/transfected with the vector and a commercial
XX test kit for determining the presence of at least one variation in a hKOR
XX gene of an allele in a bodily sample taken from a subject. The hKOR
XX variant allele is useful for determining a susceptibility in a subject to
XX at least one physiological response, condition or disease related to the
XX endogenous opioid system, nociception, neurotransmitter release
XX endogenous opioid system, learning, memory, cognition, pain, cocaine,
XX amphetamine and other stimulants self-administration, behavioural
```

CC	sensitisation to cocaine, opiates, alcohol and tobacco, opiate,
CC	amphetamine and alcohol withdrawal, physical dependence and tolerance;
CC	neuroendocrine function, reproductive function, prolactin regulation,
CC	stress responsivity, physiology and pathology of mood and affect, immune
CC	function, gastrointestinal function. The hKOR variant allele is useful
CC	for determining a susceptibility to pain in a subject and is useful for
CC	determining a therapeutically effective amount of pain reliever to
CC	administer to a subject in order to induce analgesia in the subject. The
CC	hKOR variant allele is useful for determining a therapeutically effective
CC	amount of therapeutic agent to administer to a subject suffering from at
CC	least one addictive disease to treat the at least one addictive disease.
CC	The gene for hKOR is located on chromosome 8q11.2. The present sequence
CC	is the G36T allele of hKOR.
XX	
SQ	Sequence 1154 BP; 239 A; 339 C; 286 G; 290 T; 0 U; 0 Other;
Query Match 99.7%; Score 1150.8; DB 12; Length 1154;	
Best Local Similarity 99.8%; Pred. No. 1.7e-273;	
Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
Qy	1 ATGACATCCCGATCCAGATCTTCGCGGGAGCGGGGCTACTCGCCCGAGCGCC 60
Db	
Qy	1 ATGACATCCCGATCCAGATCTTCGCGGGAGCGGGGCTACTCGCCCGAGCGCC 60
Db	
Qy	61 TGCCTGCCCCCAACAGCAGCGCGCTGTGTTCCCGGCTGGGCCGACCGCAGCAACGCG 120
Db	
Qy	61 TGCCTGCCCCCAACAGCAGCGCGCTGTGTTCCCGGCTGGGCCGACCGCAGCAACGCG 120
Db	
Qy	121 AGCGCCGGCTCGGAGGACGCGAGCTGGAGCCCGGGACATCTCCCGGCCATCCCGGTC 180
Db	
Qy	121 AGCGCCGGCTCGGAGGACGCGAGCTGGAGCCCGGGACATCTCCCGGCCATCCCGGTC 180
Db	
Qy	181 ATCATCAGCGCGGTCTACTCCGTAGTGTTCGTGTGGGCTTGGTGGGCAATCGCTGTGC 240
Db	
Qy	181 ATCATCAGCGCGGTCTACTCCGTAGTGTTCGTGTGGGCTTGGTGGGCAATCGCTGTGC 240
Db	
Qy	241 ATGTTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAATTTTAACTTTAAC 300
Db	
Qy	241 ATGTTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAATTTTAACTTTAAC 300
Db	
Qy	301 CTGGCTTTGGCAGATGCTTTAGTTACTACACCAATGCCCTTTACAGATACGGTCTACTTGG 360
Db	
Qy	301 CTGGCTTTGGCAGATGCTTTAGTTACTACACCAATGCCCTTTACAGATACGGTCTACTTGG 360
Db	
Qy	361 ATGAATTCCTGGCCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATPACTAC 420
Db	
Qy	361 ATGAATTCCTGGCCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATPACTAC 420
Db	
Qy	421 AACATGTTTACACAGCATCTTCACTTGCACCATGATGAGGTTGGAACCGCTACATTTGCCG 480
Db	
Qy	421 AACATGTTTACACAGCATCTTCACTTGCACCATGATGAGGTTGGAACCGCTACATTTGCCG 480
Db	
Qy	481 TGCCACCCCGTGAAGCTTTTGGACTTCGCGCACACCTTTGAAGGCCAAAGATCATCAATATC 540
Db	
Qy	481 TGCCACCCCGTGAAGCTTTTGGACTTCGCGCACACCTTTGAAGGCCAAAGATCATCAATATC 540
Db	
Qy	541 TGCATCTGGCTGCTGTGCGTCACTGTGTGGCATCTCTGCAATAGTCTCTGGAGGCCACCAA 600
Db	
Qy	601 GTCAGGGANGACGTGCATGTCATGAGTGCTCCTTGCAGTTCGCCAGATGATGACTACTCC 660
Db	
Qy	601 GTCAGGGANGACGTGCATGTCATGAGTGCTCCTTGCAGTTCGCCAGATGATGACTACTCC 660
Db	
Qy	661 TGGTGGGACCTCTTTCATGAAGATCTGCGTCTTTCATCTTTTGCCTTCGTGATCCCTGTCCTC 720
Db	
Qy	661 TGGTGGGACCTCTTTCATGAAGATCTGCGTCTTTCATCTTTTGCCTTCGTGATCCCTGTCCTC 720
Db	
Qy	721 ATCATCATGCTGTGCTACACCTTGATGATCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780
Db	
Qy	721 ATCATCATGCTGTGCTACACCTTGATGATCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780
Db	
Qy	781 GGTCTCCGAGAGAAAGATCGCAACCTTCGTGATGATCAACAGACTGCTGCTGGTGGTGGTG 840



XX The present invention describes antigenic peptides (1) comprising: (a)  
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
CC acids. Also described: (1) an assay for the detection of a particular G  
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
CC and (2) an isolated antibody having high specificity and high affinity or  
CC avidity for a particular GPCR. (1) can be used as GPCR modulators and in  
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an  
CC antibody against a particular GPCR, and in the production of specific  
CC antibodies. The peptides and antibodies are also useful for detecting the  
CC presence or absence of corresponding GPCRs. The antigenic peptides for  
CC GPCRs and antibodies are useful for diagnosing and designing drugs for  
CC creating immune-related diseases, growth-related diseases, cell  
CC regeneration-related disease, immunological-related cell proliferative  
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,  
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host  
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory  
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,  
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
CC any other disorder in which GPCRs are involved. The antibodies may be  
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode  
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the  
CC exemplification of the present invention  
XX

SQ Sequence 1182 BP; 245 A; 345 C; 293 G; 299 T; 0 U; 0 Other;

Query Match 99.2%; Score 1144.4; DB 8; Length 1182;  
Best Local Similarity 99.5%; Pred. No. 6.4e-272;  
Matches 1148; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGACTCCCGATCCAGATCTCCGCGGGAGCGGCGCTACTCTGCGCCCGAGCGCC 60  
Db |||||  
Qy 14 ATGAAATCCCGATTCAGATCTTCGCGGGAGCGCTGCGCCCTACTCTGCGCCCGAGCGCC 73  
Db |||||  
Qy 61 TGCTGCGCCCGCAACAGCAGCGCTGCTTCCCGGGTGGGCGGAGCGCCGAGCAACGCGC 120  
Db |||||  
Qy 74 TGCTGCGCCCGCAACAGCAGCGCTGCTTCCCGGGTGGGCGGAGCGCCGAGCAACGCGC 133  
Db |||||  
Qy 121 AGCGCGCGCTCGGAGGCGCGACCTGAGCGCGCGGAGCGCCGAGCAATCTCCCGCGGATCCCGGTC 180  
Db |||||  
Qy 134 AGCGCGCGCTCGGAGGCGCGACCTGAGCGCGCGGAGCGCCGAGCAATCTCCCGCGGATCCCGGTC 193  
Db |||||  
Qy 181 ATCATCAGCGCGGTCTACTCGTGTAGTGTTCGTCGTGGGCTTGGTGGCAACTCGCTCGTC 240  
Db |||||  
Qy 194 ATCATCAGCGCGGTCTACTCGTGTAGTGTTCGTCGTGGGCTTGGTGGCAACTCGCTCGTC 253  
Db |||||  
Qy 241 ATGTTCTGTGATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300  
Db |||||  
Qy 254 ATGTTCTGTGATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 313  
Db |||||  
Qy 301 CTGCGCTTGGCAGATGCTTTAGTACTACACATGCGCTTGGGCGGAGCGCGCTACTCTG 360  
Db |||||  
Qy 314 CTGCGCTTGGCAGATGCTTTAGTACTACACATGCGCTTGGGCGGAGCGCGCTACTCTG 373  
Db |||||  
Qy 361 ATGAATTCCTGGCGCTTTGGGGATGTGCTGTGAAGATAGTAATTTCCATTGATTACTAC 420  
Db |||||  
Qy 374 ATGAATTCCTGGCGCTTTGGGGATGTGCTGTGAAGATAGTAATTTCCATTGATTACTAC 433  
Db |||||  
Qy 421 AACATGTTCCACGACATCTTCCACCTTGACCATGATGAGCGGTGGACCGCTACATTGGCGGTG 480  
Db |||||  
Qy 434 AACATGTTCCACGACATCTTCCACCTTGACCATGATGAGCGGTGGACCGCTACATTGGCGGTG 493  
Db |||||  
Qy 481 TGCCACCGCGTGAAGGCTTTGGACTTTCGGCACACCCCTTGAAGGCAAGATCATCAATATC 540  
Db |||||  
Qy 494 TGCCACCGCGTGAAGGCTTTGGACTTTCGGCACACCCCTTGAAGGCAAGATCATCAATATC 553  
Db |||||  
Qy 541 TGCACTGCGGTGCTGCTGATCTGTTGGGATCTCTGCAATAGTCTTGGAGGCAACAAA 600  
Db |||||  
Qy 554 TGCACTGCGGTGCTGCTGATCTGTTGGGATCTCTGCAATAGTCTTGGAGGCAACAAA 613  
Db |||||

Qy 601 GTCAGGGAAGACGTCGATGTCAATGAGTGTCTTTCAGTGTCTTCCAGATGATGACTACTCC 660  
Db |||||  
Qy 614 GTCAGGGAAGACGTCGATGTCAATGAGTGTCTTTCAGTGTCTTCCAGATGATGACTACTCC 673  
Db |||||  
Qy 661 TGGTGGGACCTCTTCATGAAGATCTGGGTCTTCACTTTTGGCTTCGTGATACCTTGTCTC 720  
Db |||||  
Qy 674 TGGTGGGACCTCTTTCATGAAGATCTGGGTCTTCACTTTTGGCTTCGTGATACCTTGTCTC 733  
Db |||||  
Qy 721 ATCATCATCTGCTCTACACCTCGATGATCTCGGTCTCAAGAGCGTCCGCTCTCTTCT 780  
Db |||||  
Qy 734 ATCATCATCTGCTCTACACCTCGATGATCTCGGTCTCAAGAGCGTCCGCTCTCTTCT 793  
Db |||||  
Qy 781 GGCTCCCGAGAGAAGATCGCAACCTCGTAGGATCACAGACTGGTCTCTGGTGGTGGTG 840  
Db |||||  
Qy 794 GGCTCCCGAGAGAAGATCGCAACCTCGTAGGATCACAGACTGGTCTCTGGTGGTGGTG 853  
Db |||||  
Qy 841 GCAGTCTTCTGCTCTGAGCTCCCAATTCACATATTCATCTTCTGATGAGGCTCTGGGG 900  
Db |||||  
Qy 854 GCGGTTTTCTGCTGCTGAGCTCCCAATTCACATATTCATCTTCTGATGAGGCTCTGGGG 913  
Db |||||  
Qy 901 AGCACTCTCCACAGCAGCTGCTCTCTCCAGCTATTACTTCTGATCGGCTTAGGCTAT 960  
Db |||||  
Qy 914 AGCACTCTCCACAGCAGCTGCTCTCTCCAGCTATTACTTCTGATCGGCTTAGGCTAT 973  
Db |||||  
Qy 961 ACCAAGAGTAGCTGAATCCCAATTCCTACGCCCTTCTTGTATGAAATCTCAAGCGGTGT 1020  
Db |||||  
Qy 974 ACCAAGAGTAGCTGAATCCCAATTCCTACGCCCTTCTTGTATGAAATCTCAAGCGGTGT 1033  
Db |||||  
Qy 1021 TTCCGGGACTTCTGCTTTCACCTGAAGATGAGGATGAGCGGCGGAGCAGCTAGCAGATC 1080  
Db |||||  
Qy 1034 TTCCGGGACTTCTGCTTTCACCTGAAGATGAGGATGAGCGGCGGAGCAGCTAGCAGATC 1093  
Db |||||  
Qy 1081 CGAAATACAGTTTCAAGATCTGCTTACCTGAGGAGCATCGATGGGATGAATAAACAGTA 1140  
Db |||||  
Qy 1094 CGAAATACAGTTTCAAGATCTGCTTACCTGAGGAGCATCGATGGGATGAATAAACAGTA 1153  
Db |||||  
Qy 1141 TGACTAGTCTGGA 1154  
Db |||||  
Qy 1154 TGACTAGTCTGGA 1167  
Db |||||  
RESULT 10  
AAD58490  
ID AAD58490 standard; DNA; 1182 BP.  
XX  
AC AAD58490;  
XX  
XX 04-DEC-2003 (first entry)  
DT  
XX Human kappa opioid receptor 1 (KOR) DNA.  
DE  
XX  
XX Human; urological disorder; urinary incontinence; gene therapy; cancer;  
KW kidney disorder; overactive; oversensitive bladder; dysfunction; bladder;  
KW urethra; overflow urinary incontinence; stress urinary incontinence;  
KW nervous system; prostatitis; benign prostatic hyperplasia; nephrotrophic;  
KW kappa opioid receptor 1; KOR; gene; ds.  
XX  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH CDS 14..1156  
FT /\*tag= a  
FT /product= "Human kappa opioid receptor 1 (KOR)"  
FT /note= "The CDS is referred to as SEQ ID NO:21 in the  
FT specification"  
XX WO2003061573-A2.  
XX  
XX 31-JUL-2003.  
XX  
XX 16-JAN-2003; 2003WO-US001450.  
PF  
XX 18-JAN-2002; 2002US-0349511P.  
PR



PR 28-FEB-2002; 2002US-0360500P.  
 PR 15-MAR-2002; 2002US-0365041P.  
 PR 19-APR-2002; 2002US-0374063P.  
 PR 14-AUG-2002; 2002US-0403468P.  
 PR 27-SEP-2002; 2002US-0414262P.  
 PR 21-OCT-2002; 2002US-0419986P.  
 PR 05-NOV-2002; 2002US-0423809P.  
 PR 26-NOV-2002; 2002US-0429797P.  
 XX (MILL-) MILLENNIUM PHARM INC.  
 XX Silos-Santiago I, Karicheti V;  
 PI WPI; 2003-598705/56.  
 XX P-PSDB; AAE38589.  
 DR Identifying a compound for treating urological disorders, for example  
 PT urinary incontinence by assaying the ability of the compound to modulate  
 PT the nucleic acid expression or polypeptide activity.  
 XX Disclosure; Page 149-151; Opp; English.  
 XX The present relates to a method for identifying a compound for treating  
 CC urological disorders e.g., urinary incontinence including overactive/  
 CC over-sensitive bladder, overflow urinary incontinence, stress urinary  
 CC incontinence caused by dysfunction of the bladder, urethra or central or  
 CC peripheral nervous system, prostatitis, benign prostatic hyperplasia,  
 CC cancer of the prostate or kidney disorders. The method is also useful for  
 CC modulating hyperplasia in a cell and treating a subject having a  
 CC urological disorder. The invention is also used in gene therapy. The  
 CC present sequence is human kappa opioid receptor 1 (KOR) DNA  
 XX Sequence 1182 BP; 245 A; 345 C; 293 G; 299 T; 0 U; 0 Other;  
 SQ Query Match 99.2%; Score 1144.4; DB 10; Length 1182;  
 Best Local Similarity 99.5%; Pred. No. 6.4e-272;  
 Matches 1148; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 ATGGACTCCCGATTCAGATCTTCCGGGGAGCCGGCCCTACCTGCGCCCGGAGCGCC 60  
 DB 14 ATGGAATCCCGATTCAGATCTTCCGGGGAGCCCTGCGCCCGGAGCGCC 73  
 QY 61 TGCTGCGCCCGGATTCAGATCTTCCGGGGAGCCGGCCCTACCTGCGCCCGGAGCGCC 120  
 DB 74 TGCTGCGCCCGGATTCAGATCTTCCGGGGAGCCCTGCGCCCGGAGCGCC 133  
 QY 121 AGCGCCGGCTCGGAGGACGGCGAGCTGGAGCCCGGACATCTCCCGGCGATCCCGGTC 180  
 DB 134 AGCGCCGGCTCGGAGGACGGCGAGCTGGAGCCCGGACATCTCCCGGCGATCCCGGTC 193  
 QY 181 ATCATCAGCGGGTCTACTCGTAGTGTTCGTGGGGCTGGTGGGCACTCGCTGGTC 240  
 DB 194 ATCATCAGCGGGTCTACTCGTAGTGTTCGTGGGGCTGGTGGGCACTCGCTGGTC 253  
 QY 241 ATGTTCTGTGATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTAAAC 300  
 DB 254 ATGTTCTGTGATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTAAAC 313  
 QY 301 CTGCGTTTGGCAGATGCTTTAGTTACTACAAACGATGCGCCCTTCAGAGTACGGTCTATTG 360  
 DB 314 CTGCGTTTGGCAGATGCTTTAGTTACTACAAACGATGCGCCCTTCAGAGTACGGTCTATTG 373  
 QY 361 ATGAATTCCTGGCCCTTTGGGGATGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420  
 DB 374 ATGAATTCCTGGCCCTTTGGGGATGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 433  
 QY 421 AACATGTTTCCAGCATCTTTCACCTTGACCATGATGAGCGGTGGACCGCTACATTGCGGTG 480  
 DB 434 AACATGTTTCCAGCATCTTTCACCTTGACCATGATGAGCGGTGGACCGCTACATTGCGGTG 493  
 QY 481 TGCACCCCGGTGAAGGCTTTGGATCTTCGGCACACCCCTTGAAGGCAAGATCATCAATATC 540  
 DB 494 TGCACCCCGGTGAAGGCTTTGGATCTTCGGCACACCCCTTGAAGGCAAGATCATCAATATC 553

QY 541 TGCATCTGGCTGCTGCTGCTCATCTGTTGGCATCTCTGCAATAGTCTCTTGGAGGACACAAA 600  
 DB 554 TGCATCTGGCTGCTGCTGCTCATCTGTTGGCATCTCTGCAATAGTCTCTTGGAGGACACAAA 613  
 QY 601 GTGAGGGAAGACGTCGATGTCAATTGAGTCTCTTGGAGTCTTCCAGATGATGACTACTCC 660  
 DB 614 GTGAGGGAAGACGTCGATGTCAATTGAGTCTCTTGGAGTCTTCCAGATGATGACTACTCC 673  
 QY 661 TGGTGGGACCTTTCATGAAGATCTGCGTCTTCAATCTTGGCTTGGCTTGGATCCCTGCTC 720  
 DB 674 TGGTGGGACCTTTCATGAAGATCTGCGTCTTCAATCTTGGCTTGGCTTGGATCCCTGCTC 733  
 QY 721 ATCATCATCTGCTGCTACACCTGATGATCTTGGCTCTCAAGAGCGTCCGGCTCTCTTCT 780  
 DB 734 ATCATCATCTGCTGCTACACCTGATGATCTTGGCTCTCAAGAGCGTCCGGCTCTCTTCT 793  
 QY 781 GGCTCCCGAGAGAAAGATCGCAACCTGCTAGGATCACACAGCTGGTCTGCTGGTGGTG 840  
 DB 794 GGCTCCCGAGAGAAAGATCGCAACCTGCTAGGATCACACAGCTGGTCTGCTGGTGGTG 853  
 QY 841 GCAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
 DB 854 GCGGTTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 913  
 QY 901 AGCACCTCCACAGACAGCTGCTCTCTCCAGCTATTAATCTTGCATGCGCTTGGCTAT 960  
 DB 914 AGCACCTCCACAGACAGCTGCTCTCTCCAGCTATTAATCTTGCATGCGCTTGGCTAT 973  
 QY 961 ACCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020  
 DB 974 ACCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1033  
 QY 1021 TTCCGGGACTTCTGCTTCTTCCACTGAAGATGAGATGAGGAGCGGACAGCACTAGCAGATC 1080  
 DB 1034 TTCCGGGACTTCTGCTTCTTCCACTGAAGATGAGATGAGGAGCGGACAGCACTAGCAGATC 1093  
 QY 1081 CGAAATACAGTTTCCAGGATCTCTGCTTACCTGAGGACATCGATGGGATGAATAAACAGTA 1140  
 DB 1094 CGAAATACAGTTTCCAGGATCTCTGCTTACCTGAGGACATCGATGGGATGAATAAACAGTA 1153  
 QY 1141 TGACTAGTCTGGA 1154  
 DB 1154 TGACTAGTCTGGA 1167  
 RESULT 11  
 ADE84861  
 ID ADE84861 standard; DNA; 1182 BP.  
 XX  
 AC ADE84861;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Farnesyl transferase inhibitor modulated leukemia associated gene #80.  
 XX ss; cytostatic; farnesyl transferase inhibitor; gene expression;  
 KW quinolone; leukemia; cancer.  
 XX Homo sapiens.  
 OS  
 PN WO2003038129-A2.  
 XX  
 PD 08-MAY-2003.  
 XX  
 PF 30-OCT-2002; 2002WO-US034784.  
 XX  
 XX 30-OCT-2001; 2001US-0338997P.  
 PR 30-OCT-2001; 2001US-0340081P.  
 PR 30-OCT-2001; 2001US-0340988P.  
 PR 30-OCT-2001; 2001US-0341012P.  
 XX  
 PA (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.

XX	Raponi M;	
XX	WPI; 2003-513497/48.	
XX	Determining whether a patient will respond to treatment with a farnesyl	
XX	transferase inhibitor, by analyzing the expression of gene that is	
XX	differentially modulated in the presence of the inhibitor.	
XX	Disclosure; SEQ ID NO 80; 346pp; English.	
XX	The invention relates to a method of determining whether a patient will	
XX	respond to treatment with a farnesyl transferase inhibitor (FTI), by	
XX	analyzing the expression of gene that is differentially modulated in the	
XX	presence of an FTI. The method is useful for determining whether a	
XX	patient will respond to treatment with a FTI such as (B)-6-[amino(4-	
XX	chlorophenyl)] (1-methyl-1H-imidazol-5-yl)methyl]-4-(3-chlorophenyl)-1-	
XX	methyl-2-[1H]quinolinone, monitoring the therapy of a patient, treating a	
XX	patient with leukemia with FTI if the analysis indicates that the patient	
XX	will respond. This sequence corresponds to a gene whose expression may be	
XX	modulated in the presence of FTI.	
XX	Sequence 1182 BP; 245 A; 345 C; 293 G; 299 T; 0 U; 0 Other;	
XX	Query Match 99.2%; Score 1144.4; DB 10; Length 1182;	
XX	Best Local Similarity 99.5%; Pred. No. 6.4e-272;	
XX	Matches 1148; Conservative 0; Mismatches 6; Indels 0; Gaps 0;	
QY	1 ATGACTCCCGATCCAGATCTTCGGGGGAGCGGGCCCTACTTGGGCCCCAGGGCC 60	
DB	14 ATGGAATCCCGATTCAGATCTTCGGGGGAGCGCTGACCTGGCGCCCCAGGGCC 73	
QY	61 TGCCTGCCCGCCCAACAGCAGCGCCCTGTTTCCCGGCTGGCGCGGAGCGAGCAACGGC 120	
DB	74 TGCCTGCCCGCCCAACAGCAGCGCCCTGTTTCCCGGCTGGCGCGGAGCGAGCAACGGC 133	
QY	121 AGCGCGGCTCGAGGAGCGCGAGCTGGAGCGCGCGACATCTCCCGGCCATCCCGGTC 180	
DB	134 AGCGCGGCTCGAGGAGCGCGAGCTGGAGCGCGCGACATCTCCCGGCCATCCCGGTC 193	
QY	181 ATCATCAGCGGGTCTACTCCGTAGTGTTCGTGGGCTTGGTGGGCACTCGCTGGTC 240	
DB	194 ATCATCAGCGGGTCTACTCCGTAGTGTTCGTGGGCTTGGTGGGCACTCGCTGGTC 253	
QY	241 ATGTTCTGTGATCATCCGATACAAAGATGAAGACAGCAACCAATTTACATATTTAAC 300	
DB	254 ATGTTCTGTGATCATCCGATACAAAGATGAAGACAGCAACCAATTTACATATTTAAC 313	
QY	301 CTGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCCCTTTCAGAGTACGGTCTACTTG 360	
DB	314 CTGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCCCTTTCAGAGTACGGTCTACTTG 373	
QY	361 ATGAATTCCTGGCCTTTGGGGATGTGCTGCAAGATAGTAATTTCCATTGATTACTAC 420	
DB	374 ATGAATTCCTGGCCTTTGGGGATGTGCTGCAAGATAGTAATTTCCATTGATTACTAC 433	
QY	421 AACATGTTTACAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 480	
DB	434 AACATGTTTACAGCATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 493	
QY	481 TGCCACCCCGTGAAGGCTTTGGACTTCGCGACACCCCTTGAAGGCAAGATCATCAATATC 540	
DB	494 TGCCACCCCGTGAAGGCTTTGGACTTCGCGACACCCCTTGAAGGCAAGATCATCAATATC 553	
QY	541 TGCATCTGGCTGTGCTGTGATCTGTGGGATCTCTGCAATAGTCTTGGAGGACCAAAA 600	
DB	554 TGCATCTGGCTGTGCTGTGATCTGTGGGATCTCTGCAATAGTCTTGGAGGACCAAAA 613	
QY	601 GTACAGGGAAGACGTCGATGTCATGAGTGTCTTGGAGTTCAGAGTATGATGACTACTCC 660	
DB	614 GTACAGGGAAGACGTCGATGTCATGAGTGTCTTGGAGTTCAGAGTATGATGACTACTCC 673	
QY	661 TGGTGGGACCTCTTCATGAAGATCTGGCTCTTCATCTTTTGGCTTCGTGATCCCTGTCTC 720	
DB	674 TGGTGGGACCTCTTCATGAAGATCTGGCTCTTCATCTTTTGGCTTCGTGATCCCTGTCTC 733	
QY	721 ATCATCATCTGCTCTACACCTCTGATGATCTCTCAAGAGCGTCCGGCTCCTTTCT 780	
DB	734 ATCATCATCTGCTCTACACCTCTGATGATCTCTCAAGAGCGTCCGGCTCCTTTCT 793	
QY	781 GGCTCCCGAGAGAAAGATCGCAACCTCGTAGGATCACAGACTGGTCTCTGGTGGTGTG 840	
DB	794 GGCTCCCGAGAGAAAGATCGCAACCTCGTAGGATCACAGACTGGTCTCTGGTGGTGTG 853	
QY	841 GCAGTCTTCTGTTGCTCTGAGACTCCCATTCACATATTCATCTCTGGTGGAGGCTCTGGGG 900	
DB	854 GCGGTTTTTCTGCTCTGAGACTCCCATTCACATATTCATCTCTGGTGGAGGCTCTGGGG 913	
QY	901 AGCACTCCACACAGCAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCTTAGGCTAT 960	
DB	914 AGCACTCCACACAGCAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCTTAGGCTAT 973	
QY	961 ACCAACAGTAGCTGAATCCCATTTCTTAGCGCTTTTCTTGATGAAACTTCAAGCGGTGT 1020	
DB	974 ACCAACAGTAGCTGAATCCCATTTCTTAGCGCTTTTCTTGATGAAACTTCAAGCGGTGT 1033	
QY	1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGCGGCAGAGCACTAGCAGAGTC 1080	
DB	1034 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGCGGCAGAGCACTAGCAGAGTC 1093	
QY	1081 CGAAATACAGTTCAAGGATCTGCTTACCTGAGGACATCGATGGGATGAATAAACCACTA 1140	
DB	1094 CGAAATACAGTTCAAGGATCTGCTTACCTGAGGACATCGATGGGATGAATAAACCACTA 1153	
QY	1141 TGACTAGTCTGTGA 1154	
DB	1154 TGACTAGTCTGTGA 1167	
XX	RESULT 12	
XX	ACAS6819	
XX	ID ACAS6819 standard; cDNA; 1182 BP.	
XX	AC ACAS6819;	
XX	XX 06-JUN-2003 (first entry)	
XX	DT Human signalling pathway polynucleotide probe SEQ ID NO 1417.	
XX	DE Human; probe; ss; array element; Parkinson's disease;	
XX	KW signalling pathway population; cancer; adenocarcinoma; leukaemia;	
XX	KW immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.	
XX	OS Homo sapiens.	
XX	XX US6500938-B1.	
XX	XX 31-DEC-2002.	
XX	XX 30-JAN-1998; 98US-00016434.	
XX	XX 30-JAN-1998; 98US-00016434.	
XX	XX (INCY-) INCYTE GENOMICS INC.	
XX	XX Au-Young J, Seilhamer JJ;	
XX	XX WPI; 2003-352189/33.	
XX	XX Combination of polynucleotide probes, useful as array elements in a	
XX	XX microarray for monitoring the expression of a number of target	
XX	XX polynucleotides.	
XX	XX Claim 1; SEQ ID NO 1417; 65pp; English.	
XX	XX The invention relates to a combination which, comprises a number of	
XX	CC	

CC polynucleotide probes comprising a sequence selected from one of the 1490  
CC sequences mentioned in the specification. The combination is useful as an  
CC array element in a microarray for monitoring the expression of a number  
CC of target polynucleotides. The microarray is particularly useful in the  
CC diagnosis and treatment of cancer and immunopathology and neuropathology.  
CC The microarray is useful in diagnostics and treatment regimens, drug  
CC discovery and development, toxicological and carcinogenicity studies,  
CC forensics and pharmacogenomics. The microarray is also useful for  
CC monitoring progression of diseases and for developing sophisticated  
CC profiles for the effects of currently available therapeutic drugs. The  
CC combination is also useful for purifying a subpopulation of mRNAs, cDNAs  
CC and genomic fragments and in research and diagnostic applications. The  
CC array can detect changes in expression in a large number of genes coding  
CC for different signaling pathway populations which can be used to diagnose  
CC various diseases including cancer e.g. adenocarcinoma and leukemia,  
CC immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease  
CC and Parkinson's disease. The present sequence represents a polynucleotide  
CC probe of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html?docID=06500938B1  
XX  
SQ Sequence 1182 BP; 245 A; 345 C; 293 G; 299 T; 0 U; 0 Other;

[illegible]

RESIT.T 13

RESUL I  
ADT56615

AD156615  
ID AD156615 standard: DNA: 1182 BP.

AA ADI56615;  
AC

DT 22-APR-2004 (first entry)

XX  
DE Human polynucleotide probe #1417.

Human; probe; ss; receptor-like polypeptide; transducing polypeptide;  
effector-like polypeptide; cancer; immunopathology; neuropathology;  
drug development; toxicology; carcinogenicity;  
signalling pathway polypeptide; adrenal gland; bladder; bone;  
bone marrow; brain; breast; cervix; tumour; immunopathology; AIDS;  
diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology  
dementia; amnesia; encephalitis; Alzheimer's disease; depression.

XX Homo sapiens.

XX  
PN  
IIS2004010136-A1XX  
15-JAN-2004  
RDXX  
26-NOV-2002. 2002US-00305720.XX  
BB 30-JAN-1988. 98HS-00016434XX  
BA (TNCV-) TNCVTE GENOMICS TNCXX  
BT  
Lu-Young J. Seilhamer JJ.XX  
WBT: 2004-090520/09  
DB

XX New composition comprising polynucleotide probes, useful as array  
PT elements in a microarray for monitoring the expression of target  
PT polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic

fragments.

Claim 6; SEQ ID NO 1417; 73pp; English.

The invention relates to a composition of polynucleotide probes comprising first polynucleotide probes comprising at least a portion of a gene encoding a receptor-like polypeptide, second polynucleotide probes comprising at least a portion of a gene encoding a transducing polypeptide and third polynucleotide probes comprising at least a portion of a gene encoding an effector-like polypeptide. The probes of the composition are useful as array elements in a microarray for monitoring the expression of target polynucleotides. The microarray is useful in the diagnosis and treatment of cancer, an immunopathology or a neuropathology. It can also be used for drug discovery and development, toxicological and carcinogenicity studies, forensics or pharmacogenomics. Microarrays can also be used for monitoring the progression of diseases that may be associated with the altered expression of signalling pathway polypeptides. The composition can also be used to purify a subpopulation of mRNAs, cDNAs, or genomic fragments in a sample. The expression profile is also useful for the diagnosis and treatment of cancer, e.g. cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix, an immunopathology, e.g. AIDS, diabetes, pancreatitis, osteoporosis or ulcerative colitis, or a neuropathology, e.g. dementia, amnesia, epilepsy, Alzheimer's disease or depression. This sequence represents a human polynucleotide probe of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).

Sequence 1182 BP; 245 A; 345 C; 293 G; 299 T; 0 U; 0 Other;

Query Match 99.2%; Score 1144.4; DB 12; Length 1182;

Best Local Similarity 99.5%; Pred. No. 6.4e-272; Matches 1148; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy	1	ATGACTCTCCCGATCCAGATCTTCGCGGGGAGCGGGCCCTACTCTGCGCCCCGAGCGCC	60
Db	14	ATGAATATCCCGATTCAGATCTTCGCGGGGAGCGGGCCCTACTCTGCGCCCCGAGCGCC	73
Qy	61	TGCTGCGCCCCCAACAGCAGCGCTGTTTCCCGGGTGGCGCGAGCCCGCAGCAACGGC	120
Db	74	TGCTGCGCCCCCAACAGCAGCGCTGTTTCCCGGGTGGCGCGAGCCCGCAGCAACGGC	133
Qy	121	AGCGCGGCTCGGAGGAGCGCAGCTGGAGCGCCGCGCACATCTCCCGGCCCATCCCGGTC	180
Db	134	AGCGCGGCTCGGAGGAGCGCAGCTGGAGCGCCGCGCACATCTCCCGGCCCATCCCGGTC	193
Qy	181	ATCATCAGCGGGTCTACTCGTAGTGTTCGTGCGGGTGGTGGGCAATCTCGTGGTC	240
Db	194	ATCATCAGCGGGTCTACTCGTAGTGTTCGTGCGGGTGGTGGGCAATCTCGTGGTC	253
Qy	241	ATGTTGTGTATCATCCGATACACAAAGATGAAGACAGCAACCAATTTACATATTAAC	300
Db	254	ATGTTGTGTATCATCCGATACACAAAGATGAAGACAGCAACCAATTTACATATTAAC	313
Qy	301	CTGCGTTTGGCAGATGCTTTAGTTACTACACACCATGCGCTTTTCAGAGTACGGTCTACTTG	360
Db	314	CTGCGTTTGGCAGATGCTTTAGTTACTACACACCATGCGCTTTTCAGAGTACGGTCTACTTG	373
Qy	361	ATGAATTCCTGGCCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC	420
Db	374	ATGAATTCCTGGCCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC	433
Qy	421	AACATGTTCCACAGCATCTTCACTTGCACCATGATGAGCGTGGACCGCTACATTCGCGTG	480
Db	434	AACATGTTCCACAGCATCTTCACTTGCACCATGATGAGCGTGGACCGCTACATTCGCGTG	493
Qy	481	TGCCACCCCGTGAAGGGCTTTGGAATTCGCGCACACCTTTGAAGGCAAGATCATCAATATC	540
Db	494	TGCCACCCCGTGAAGGGCTTTGGAATTCGCGCACACCTTTGAAGGCAAGATCATCAATATC	553
Qy	541	TGCATCTGGCTGTCTCGTCACTCTGTGGCATCTCTGCAATAGTCTTGGAGGACCAAA	600

Db	554	TGCATCTGGCTGTCTCGTCACTCTGTGGCATCTCTGCAATAGTCTTGGAGGACCAAA	613
Qy	601	GTCAAGGAAGACGTCGATGTCATTCAGTGTCTCTTCAGTTCCTCCAGATGATGACTACTCC	660
Db	614	GTCAAGGAAGACGTCGATGTCATTCAGTGTCTCTTCAGTTCCTCCAGATGATGACTACTCC	673
Qy	661	TGTTGGGACCTCTTCATGAAGATCTGGGTCTTCATCTTTGCTTTCGATGATCCCTGTCTC	720
Db	674	TGTTGGGACCTCTTCATGAAGATCTGGGTCTTCATCTTTGCTTTCGATGATCCCTGTCTC	733
Qy	721	ATCATCATCTCTGCTACACCCCTGATGATCTCGGTCTCAAGAGCGTCCGCTCTCTTCT	780
Db	734	ATCATCATCTCTGCTACACCCCTGATGATCTCGGTCTCAAGAGCGTCCGCTCTCTTCT	793
Qy	781	GGCTCCCGAGAGAAGATCGCAACTCGTAGGATCACAGACTGGTCTCTGTTGGTGTG	840
Db	794	GGCTCCCGAGAGAAGATCGCAACTCGTAGGATCACAGACTGGTCTCTGTTGGTGTG	853
Qy	841	GCAGTCTTCGTGTCTCTCGACTCCCATTCACATATTCATCTCTGTTGGAGGCTCTGGGG	900
Db	854	GCAGTCTTCGTGTCTCTCGACTCCCATTCACATATTCATCTCTGTTGGAGGCTCTGGGG	913
Qy	901	AGCACCTCCACACAGCAGCTGCTCTCCAGCTATTACTTCTGCATCGCTTAGGCTAT	960
Db	914	AGCACCTCCACACAGCAGCTGCTCTCCAGCTATTACTTCTGCATCGCTTAGGCTAT	973
Qy	961	ACCAACAGTAGCTGAATCCCATTTCTAGCGCTTTCTTGATGAAAATCTCAAGCGGTGT	1020
Db	974	ACCAACAGTAGCTGAATCCCATTTCTAGCGCTTTCTTGATGAAAATCTCAAGCGGTGT	1033
Qy	1021	TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGCGGCGCAGACACTAGCAGATC	1080
Db	1034	TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGCGGCGCAGACACTAGCAGATC	1093
Qy	1081	CGAATACAGTTACAGATCTCTTACTCTGAGGACATCGATGGGATGAATAAACAGTA	1140
Db	1094	CGAATACAGTTACAGATCTCTTACTCTGAGGACATCGATGGGATGAATAAACAGTA	1153
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AAT90998			
ID	AAT90998 standard; cDNA; 1143 BP.		
XX	AAT90998;		
AC	AAT90998;		
XX	14-APR-1998 (first entry)		
DT	Human kappa opioid receptor cDNA.		
XX	Human kappa opioid receptor cDNA.		
DE	Selective target cell activation; G protein-coupled receptor; RASL;		
XX	gene therapy; cell proliferation; kappa opioid receptor; human;		
KW	transgenic animal; arrhythmia; bone disease; seizure;		
KW	vascular contraction; disease model; ss.		
OS	Homo sapiens.		
XX	WO9735478-A1.		
PN	02-OCT-1997.		
XX	25-MAR-1997; 97WO-US005334.		
XX	26-MAR-1996; 96US-00622348.		
PF	(REGC ) UNIV CALIFORNIA.		
XX	Conklin BR;		
PI	WPI; 1997-502739/46.		
XX			
DR			



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PN WO9601898-Al.
XX
XX PD 25-JAN-1996.
XX
XX PF 07-JUL-1995; 95WO-FR000912.
XX
XX PR 11-JUL-1994; 94FR-00008531.
XX
XX PA (UYST-) UNIV PASTEUR STRASBOURG LOUIS.
XX
XX PI Kieffer B, Simonin F;
XX
XX DR WPI; 1996-097628/10.
XX
XX DR P-PSDB; AAR88722.
XX
XX
XX PT New nucleic acid encoding the human Kappa opioid receptor - useful in
XX diagnosis and therapy, and for isolating receptor ligands and modulators.
XX
XX PS Claim 3; Page 13-15; 30pp; French.
XX
XX CC This sequence codes for the human kappa opioid receptor and was obtained
XX from two overlapping cDNA fragments isolated from a human placental cDNA
XX library. The fragments were amplified from the library using PCR primers
XX based on the sequence of human genomic clones which hybridised with a
XX murine delta receptor cDNA probe. Nucleotide probes derived from the
XX kappa opioid receptor coding sequence are useful for diagnosis of
XX neurological, cardio-vascular and psychiatric disorders associated with
XX opioid receptors
XX
XX SQ Sequence 1142 BP; 236 A; 337 C; 283 G; 286 T; 0 U; 0 Other;

Query Match 98.8%; Score 1140.4; DB 2; Length 1142;
Best Local Similarity 99.9%; Pred. No. 6.1e-271;
Matches 1141; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 ATGACTCCCGATCCAGATCTTCGGGGGAGCGGGCCCTACCTGGCCCCCGAGCGCC 60
Qy 61 TGCCTGCCCGCCCAACAGCAGCGCTGTTTCCGGCTGGGCGGAGCGCCGAGCAACGGC 120
Db 61 TGCCTGCCCGCCCAACAGCAGCGCTGTTTCCGGCTGGGCGGAGCGCCGAGCAACGGC 120
Qy 121 AGCGCGGCTCGGAGGAGCGCAGCTGGAGCGCGGAGCGCCGAGCAATCCCGGTC 180
Db 121 AGCGCGGCTCGGAGGAGCGCAGCTGGAGCGCGGAGCGCCGAGCAATCCCGGTC 180
Qy 181 ATCATCAGCGCGTCTACTCCGTAGTGTTCGTGGGCTTGGTGGGCAACTCGCTGTC 240
Db 181 ATCATCAGCGCGTCTACTCCGTAGTGTTCGTGGGCTTGGTGGGCAACTCGCTGTC 240
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Db 241 ATGTTCTGTGATCCCGATACACAAGATGAGCAGCAACCAATTTACATATTAAAC 300
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Db 361 ATGAATTCCTGGCCTTTTGGGGATGTGCTGTCGAAGATAGTAAATTCATTGATTACTAC 420
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Db 421 AACATGTTCCACGAGATCTTACCTTGACCATGATGAGCGTGGACCGGTACATTGCCGTG 480
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Db 481 TGCCACCCCGTGAAGGCTTTGAGCTTCGCGACACCCCTTGAAGGCAAGATCATCAATATC 540
Qy 541 TGCATCTGGCTGTGTCGTCTCTGTTGGCATCTCTGCAATAGTCTTGGAGGCCACCAA 600
Db 541 TGCATCTGGCTGTGTCGTCTCTGTTGGCATCTCTGCAATAGTCTTGGAGGCCACCAA 600

601 GTGAGGGAAGACGTCGATGTCAATTGAGTGTCTCTTGCAGTTCCAGATGATGACTACTCC 660
601 GTGAGGGAAGACGTCGATGTCAATTGAGTGTCTCTTGCAGTTCCAGATGATGACTACTCC 660
661 TGGTGGGACCTCTTTCATGAAGATCGCGTCTTCATCTTTCGCTTTCGTCGTCCTC 720
661 TGGTGGGACCTCTTTCATGAAGATCGCGTCTTCATCTTTCGCTTTCGTCGTCCTC 720
721 ATCATCATCTGCTCTACACCCCTGATGATCTGCGTCTCAAGAGGCTCCGGCTCTTCT 780
721 ATCATCATCTGCTCTACACCCCTGATGATCTGCGTCTCAAGAGGCTCCGGCTCTTCT 780
781 GGCTCCCGAGAGAAAGATCGCAACTCGGTAGGATCACAGACTGGTCTCTGGTGGTGTG 840
781 GGCTCCCGAGAGAAAGATCGCAACTCGGTAGGATCACAGACTGGTCTCTGGTGGTGTG 840
841 GCAGTCTTTCGTTGTCTGCTGGACTCCCATTCACATATTCATCTCTGGTGGAGGCTCTGGGG 900
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901 AGCACTCCCGACAGCAGCTGCTCTCTCAGCTATTACTTCTGATCGCCTTAGGCTAT 960
901 AGCACTCCCGACAGCAGCTGCTCTCTCAGCTATTACTTCTGATCGCCTTAGGCTAT 960
961 ACCAACAGTAGCCCTGAATCCCATTTCTACGCCCTTCTTGTATGAAACTTCAAGCGGTG 1020
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OM nucleic - nucleic search, using sw model

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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 6: /cgn2\_6/ptodata/1/ina/backfiles.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1144.4	99.2	1182	4	US-09-016-434-1417
2	1141.4	98.9	1143	4	US-09-341-446B-1
3	1140.4	98.8	1142	3	US-08-765-743-1
4	1136.2	98.5	1284	4	US-09-341-446B-3
5	1130.2	97.9	1143	4	US-09-826-509-542
6	999.4	86.6	1275	4	US-09-341-446B-5
7	994.6	86.2	1275	4	US-09-341-446B-7
8	909.2	78.8	1408	4	US-09-214-904-5
9	909.2	78.8	1410	3	US-08-147-592A-1
10	909.2	78.8	1410	3	US-08-292-694A-1
11	869.6	75.4	1000	3	US-08-147-592A-11
12	869.6	75.4	1000	3	US-08-292-694A-11
13	446.4	38.7	2135	3	US-08-430-286A-1
14	444.8	38.5	1618	3	US-08-889-108-1
15	444.8	38.5	1618	3	US-08-889-108-3
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19	444.8	38.5	1618	5	PCT-US94-10358-3
20	434	37.6	1334	4	US-09-761-962A-3
21	434	37.6	1365	4	US-09-761-962A-11
22	434	37.6	1423	4	US-09-761-962A-1
23	434	37.6	1610	4	US-09-761-962A-16
24	434	37.6	1729	4	US-09-761-962A-9
25	434	37.6	2045	4	US-09-761-962A-10
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27	433.2	37.5	1610	5	PCT-US94-10358-7

28 433.2 37.5 2160 3 US-08-188-275A-1  
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30 433.2 37.5 2162 3 US-09-113-426-1  
31 433.2 37.5 2162 4 US-09-016-434-1379  
32 433.2 37.5 2162 4 US-09-355-709C-7  
33 432.4 37.5 2229 4 US-09-214-904-1  
34 430.8 37.3 1542 4 US-09-761-962A-4  
35 430.8 37.3 1981 3 US-08-387-707-15  
36 430.8 37.3 1981 3 US-08-405-271A-15  
37 430 37.3 1182 4 US-09-826-509-546  
38 430 37.3 1203 4 US-09-826-509-544  
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44 422.6 36.6 2272 3 US-08-147-592A-3  
45 422.6 36.6 2272 3 US-08-292-694A-3

## ALIGNMENTS

RESULT 1  
US-09-016-434-1417  
; Sequence 1417, Application US/09016434  
; Patent No. 6500938  
; GENERAL INFORMATION:  
; APPLICANT: Janice Au-Young  
; APPLICANT: Jeffrey J. Sellhammer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1490  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/016,434  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0002 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 1417:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1182 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: 9532059  
; US-09-016-434-1417

Query Match 99.2%; Score 1144.4; DB 4; Length 1182;  
Best Local Similarity 99.5%; Pred. No. 1.8e-274;

Matches 1148; Conservative 0; Mismatches 6; Indels 0; Gaps 0;	
Qy	1 ATGAGATCCCGCATCAGATCTTCCGCGGGAGCGGGCCCTACCTGCGCCCCGAGCGCC 60
Db	14 ATGGAATCCCGATTAGATCTTCCGCGGGAGCTGGCCCTACCTGGCCCCGAGCGCC 73
Qy	61 TGCCTGCCCCCAAAGCAGCGCTGGTTTCCGGCTGGCGCGAGCCCGACAGCAACGCG 120
Db	74 TGCCTGCCCCCAAAGCAGCGCTGGTTTCCGGCTGGCGCGAGCCCGACAGCAACGCG 133
Qy	121 AGCGCGGCTCGAGGACGCGCAGCTGGAGCCCGCGCACATCTCCCGGCCATCCCGGTC 180
Db	134 AGCGCGGCTCGAGGACGCGCAGCTGGAGCCCGCGCACATCTCCCGGCCATCCCGGTC 193
Qy	181 ATCATCAGCGCGCTCTACTCCGTAAGTCTGCTGGGGCTTGGTGGGCAACTCGCTGTC 240
Db	194 ATCATCAGCGCGCTCTACTCCGTAAGTCTGCTGGGGCTTGGTGGGCAACTCGCTGTC 253
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Db	254 ATGTTCTGTGATCATCCGATACACAAAGATGAAGACAGCAACCAATTTACATATTAA 313
Qy	301 CTGCGTTTGGCAGATGCTTTAGTTACTACAAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
Db	314 CTGCGTTTGGCAGATGCTTTAGTTACTACAAACCATGCCCTTTCAGAGTACGGTCTACTTG 373
Qy	361 ATGAATCTCGGCCCTTTTGGGGATGTCTGTGCAAGATAGTAATTTCCATTTGATTACTAC 420
Db	374 ATGAATCTCGGCCCTTTTGGGGATGTCTGTGCAAGATAGTAATTTCCATTTGATTACTAC 433
Qy	421 AACATGTTCAACAGCATCTTACCTTGACCATGATGAGCGTGGACCGCTACATGCGCGTG 480
Db	434 AACATGTTCAACAGCATCTTACCTTGACCATGATGAGCGTGGACCGCTACATGCGCGTG 493
Qy	481 TGCACACCGGTGAAGGCTTTGGACTTCGCGACACCCCTTGAAGCGAAAGATCATCAATATC 540
Db	494 TGCACACCGGTGAAGGCTTTGGACTTCGCGACACCCCTTGAAGCGAAAGATCATCAATATC 553
Qy	541 TGCATCTGGCTGCTGTGGTCTATCTGTTTGGCACTCTCTGCAATAGTTCCTTGAGGACCAAA 600
Db	554 TGCATCTGGCTGCTGTGGTCTATCTGTTTGGCACTCTCTGCAATAGTTCCTTGAGGACCAAA 613
Qy	601 GTCAGGGAAGAGTCGATGTCAATTGAGTGCTCTTGCAGTTCCTCCAGATGATGACTACTCC 660
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Qy	661 TGTGTGGACCTCTTCATGAAGATCTGGCTCTTTCATCTTTGCTTCGTGATCCCTGCTCCTC 720
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Qy	781 GGCTCCGAGGAAGAATCGCAACCTCGTAGGATCACAGACTGTGCTCTGGTGGTGGTG 840
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Qy	841 GCAGTCTTCGTGTTCTGTGGACTCCCATTCACATATTTCATCTGTTGGAGGCTCTGGGG 900
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Db	974 ACCAACAGTAGCCTGAAATCCCATTTCTACGCGCTTTCTTGATGAAATCTTCAACGCGTGT 1033
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Oy 1081 CGAAATACAGTTCAGGATCTCTGCTTACCTCAGGAGACATCGATGGATGAATAAACCACTGA 1144
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Oy 1141 TGACTAGTCGTGGA 1154
Db 1154 TGACTAGTCGTGGA 1167

RESULT 2
US-09-341-446B-1
; Sequence 1, Application US/09341446B
; Patent No. 6518480
; GENERAL INFORMATION:
; APPLICANT: Conklin, Bruce R.
; TITLE OF INVENTION: Selective Target Cell Activation By
; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated
; TITLE OF INVENTION: Superiorly By Synthetic Ligand
; FILE REFERENCE: UCAL-049CIP
; CURRENT APPLICATION NUMBER: US/09/341.446B
; CURRENT FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US97/05334
; PRIOR FILING DATE: 1997-03-25
; PRIOR APPLICATION NUMBER: US 08/622,348
; PRIOR FILING DATE: 1996-03-26
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1143
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-341-446B-1

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Db	661		720	QY	122	GGCCCGGCTCGAGGACGGCGAGCTGGAGCCGCGCAGATCTCCCGCGCATCCCGGTCA	181
QY	721	ATCATCATCGTCTGTCTACACCTGTATGATCTGGCTCTCAAGAGCGTGGGCTCTTTCT	780	Db	233	GGCCCGGCTCGAGGACGGCGAGCTGGAGCCGCGCAGATCTCCCGCGCATCCCGGTCA	292
Db	721		780	QY	182	TCATCAGCGGCTCTACTCCGTAGTGTCTGGTGGGCTTGGTGGGCAACTCGCTGGTCA	241
QY	781	GGCTCCGAGAGAAAGATCGCAACCTGCTAGGATCACCAGACTGGTCTGGTGGTGGT	840	Db	293	TCATCAGCGGCTCTACTCCGTAGTGTCTGGTGGGCTTGGTGGGCAACTCGCTGGTCA	352
Db	781		840	QY	242	TGTTGCTGATCATCCGATACACAAAGATGAAGACAGCAACCAATTTACATTTAAACC	301
QY	841	GCAGTCTTCTGTCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	900	Db	353	TGTTGCTGATCATCCGATACACAAAGATGAAGACAGCAACCAATTTACATTTAAACC	412
Db	841		900	QY	302	TGGCTTTGGCAGATGCTTTTGTAGTTACTACAAACCATGCCCTTTCAGAGTACGGTCTACTTGA	361
QY	901	AGCACTTCCACAGCAGCTGCTCTCTCCAGCTATTTCTTGCATCGCTTACGCTAT	960	Db	413	TGGCTTTGGCAGATGCTTTTGTAGTTACTACAAACCATGCCCTTTCAGAGTACGGTCTACTTGA	472
Db	901		960	QY	362	TGAATTCCTGGCCCTTTTGGGATGTCTGTCAAGATAGTAAATTCATTGATTTACTACA	421
QY	961	ACCAACAGTACCTGAACTCCATCTCTACGCCCTTTCTTGATGAAATTTCAAGCGGT	1020	Db	473	TGAATTCCTGGCCCTTTTGGGATGTCTGTCAAGATAGTAAATTCATTGATTTACTACA	532
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				Db	713	TCAGGAGAGCGTGATGCTCATTCAGTGTCTCTTTCAGTGTCTCCAGATGATGATCTCT	772
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				Db	773	GGTGGGACCTCTTTCATGAAGATCTGGCTTTCATCTTTGGCTTCTGATCCCTGCTCA	832
				QY	722	TCATCATCTGTCTGTCTACACCTGTATGCTGCTCTCAAGAGCGTCCGGCTCTCTTCTG	781
				Db	833	TCATCATCTGTCTGTCTACACCTGTATGCTGCTCTCAAGAGCGTCCGGCTCTCTTCTG	892
				QY	782	GCTCCCGAGAGAAAGATCGCAACCTCGGTAGGATCACAGACTGGTCTCTGGTGGTGG	841
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				QY	842	CAGTCTTCTGTCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	901
				Db	953	CAGTCTTCTGTCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1012
				QY	902	GCACCTCCACAGCAGCTGCTCTCTCCAGCTATTTACTTCTGCAATCGCTTACGCTATA	961
				Db	1013	GCACCTCCACAGCAGCTGCTCTCTCCAGCTATTTACTTCTGCAATCGCTTACGCTATA	1072
				QY	962	CCAACAGTAGCTGAATCCCATTTCTTACGCTTCTTCTGATGAAACTTCAAGCGGTGT	1021
				Db	1073	CCAACAGTAGCTGAATCCCATTTCTTACGCTTCTTCTGATGAAACTTCAAGCGGTGT	1132
				QY	1022	TCGGGACCTTCTGCTTTTCCACTGAAAGATGAGGATGAGCGGAGAGCACTAGCAGATCC	1081
				Db	1133	TCGGGACCTTCTGCTTTTCCACTGAAAGATGAGGATGAGCGGAGAGCACTAGCAGATCC	1192
				QY	1082	GAAATACAGTTCAGGATCTCTGCTTACCTGAGGACATCCGATGGATGAATTAACAGTAT	1141
				Db	1193	GAAATACAGTTCAGGATCTCTGCTTACCTGAGGACATCCGATGGATGAATTAACAGTAT	1252
				QY	1142	G 1142	
				Db	1253	G 1253	

RESULT 4  
US-09-341-446B-3  
; Sequence 3, Application US/09341446B  
; Patent No. 6518480  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Bruce R.  
; TITLE OF INVENTION: Selective Target Cell Activation By  
; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated  
; TITLE OF INVENTION: Superiorly By Synthetic Ligand  
; FILE REFERENCE: UCAL-049CIP  
; CURRENT APPLICATION NUMBER: US/09/341.446B  
; PRIORITY FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US97/05334  
; PRIOR FILING DATE: 1997-03-25  
; PRIOR APPLICATION NUMBER: US 08/622,348  
; PRIOR FILING DATE: 1996-03-26  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1284  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: modified KOR  
US-09-341-446B-3

Query Match 98.5%; Score 1136.2; DB 4; Length 1284;  
Best Local Similarity 99.7%; Pred. No. 28-272; Indels 0; Gaps 0;  
Matches 1138; Conservative 0; Mismatches 3;  
QY 2 TGGACTCCCGATCCAGATCTTCCGCGGGAGCCCGGCGCTTACTCTGCGCCCGAGCGCT 61  
Db 113 TCGACTCCCGATCCAGATCTTCCGCGGGAGCCCGGCGCTTACTCTGCGCCCGAGCGCT 172  
QY 62 GCTGCGCCCGAACAGCAGCGCTGCTTCCGCGCTGGCGGAGCCCGAGCAACAGCA 121

RESULT 5  
 US-09-826-509-542  
 ; Sequence 542, Application US/09826509  
 ; Patent No. 6806054  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lehmann-Bruinsma, Karin  
 ; APPLICANT: Liaw, Chen W.  
 ; APPLICANT: Lin, I-Lin  
 ; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G  
 ; FILE REFERENCE: ARN-207  
 ; CURRENT APPLICATION NUMBER: US/09/826,509  
 ; CURRENT FILING DATE: 2001-04-05  
 ; PRIOR APPLICATION NUMBER: 60/195,747  
 ; PRIOR FILING DATE: 2000-04-07  
 ; PRIOR APPLICATION NUMBER: 09/170,496  
 ; PRIOR FILING DATE: 1998-10-13  
 ; NUMBER OF SEQ ID NOS: 589  
 ; SOFTWARE: Patent In Version 2.1  
 ; SEQ ID NO 542  
 ; LENGTH: 1143  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-826-509-542  
 Query Match 97.9%; Score 1130.2; DB 4; Length 1143;  
 Best Local Similarity 99.3%; Pred. No. 6e-271;  
 Matches 1135; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
 Qy 1 ATGACTCCCCGATCCAGATCTTCGCGGGGAGCGGGCCCTACTGCGCCCGCGAGCGCC 60  
 Db 1 ATGGAATCCCCGATTCAGATCTTCGCGGGGAGCGCTGCGCCCTACTGCGCCCGCGAGCGCC 60  
 Qy 61 TGCCTGCCCCCAACAGCAGCGCGCTGTTTCCCGGTGGCGGAGCGCCGAGCGCAACAGCGC 120  
 Db 61 TGCCTGCCCCCAACAGCAGCGCGCTGTTTCCCGGTGGCGGAGCGCGCTGCGCCCGCGAGCGCC 120  
 Qy 121 AGCGCGGCTCGGAGGAGCGCGAGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180  
 Db 121 AGCGCGGCTCGGAGGAGCGCGAGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180  
 Qy 181 ATCATCAGCGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGTGGGCAACTCGCTGGTC 240  
 Db 181 ATCATCAGCGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGTGGGCAACTCGCTGGTC 240  
 Qy 241 ATGTTCTGTATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300  
 Db 241 ATGTTCTGTATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300  
 Qy 301 CTGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCGGCGGCGGCGGCGGCGGCGGCGG 360  
 Db 301 CTGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCGGCGGCGGCGGCGGCGGCGGCGG 360  
 Qy 361 ATGAATCTCGGCTTTGGGCGATGCTGTGCAAGATAGTAATTTCAATTTGATTTACTAC 420  
 Db 361 ATGAATCTCGGCTTTGGGCGATGCTGTGCAAGATAGTAATTTCAATTTGATTTACTAC 420  
 Qy 421 AACATGTTACAGATCTTCACTTACCATGATGAGCGTGGACCGGCTACATTTGCGGTG 480  
 Db 421 AACATGTTACAGATCTTCACTTACCATGATGAGCGTGGACCGGCTACATTTGCGGTG 480  
 Qy 481 TGCCACCGCGTGAAGGCTTTGGATTCGCGACACCCCTTGAGGCAAGATCATCAATATC 540  
 Db 481 TGCCACCGCGTGAAGGCTTTGGATTCGCGACACCCCTTGAGGCAAGATCATCAATATC 540  
 Qy 541 TGCACTGCGCTGCTGCTCATCTGTGGCATCTCTGCAATAGTCTTGGAGGACCAAA 600  
 Db 541 TGCACTGCGCTGCTGCTCATCTGTGGCATCTCTGCAATAGTCTTGGAGGACCAAA 600  
 Qy 601 GTCAGGGAAGACGTGCGATGTCATTTAGTGTCTTTCGAGTTCCAGATGATGACTATCC 660  
 Db 601 GTCAGGGAAGACGTGCGATGTCATTTAGTGTCTTTCGAGTTCCAGATGATGACTATCC 660

Db 601 GTCAGGGAAGACGTGCGATGTCATTTAGTGTCTTTCGAGTTCCAGATGATGACTATCC 660  
 Qy 661 TGGTGGACCTCTTCATGAAGATCTGGCTCTTTCATCTTTTGGCTTTCGATGATCCCTGTCTCTC 720  
 Db 661 TGGTGGACCTCTTCATGAAGATCTGGCTCTTTCATCTTTTGGCTTTCGATGATCCCTGTCTCTC 720  
 Qy 721 ATCATCATCGTCTCTACACCCCTGATGATCTCGGCTCTCAAGAGCGTCCGGCTCTCTTTCT 780  
 Db 721 ATCATCATCGTCTCTACACCCCTGATGATCTCGGCTCTCAAGAGCGTCCGGCTCTCTTTCT 780  
 Qy 781 GGCTCCCGAGAGAAGATCGCAACCTCGTAGGATCAAGAGACTGGTCTCTGGTGGTG 840  
 Db 781 GGCTCCCGAGAGAAGATCGCAACCTCGTAGGATCAAGAGACTGGTCTCTGGTGGTG 840  
 Qy 841 GCAGTCTTCTGCTGCTGAGCTCCCATTCACATATTCATCTTGGTGGAGGCTCTTGGGG 900  
 Db 841 GCGGTTTTGCTGCTGCTGAGCTCCCATTCACATATTCATCTTGGTGGAGGCTCTTGGGG 900  
 Qy 901 AGCACTTCCACAGCAGCTGCTCTCCAGCTTATTTACTTCTCATCGCTTAGGCTAT 960  
 Db 901 AGCACTTCCACAGCAGCTGCTCTCCAGCTTATTTACTTCTCATCGCTTAGGCTAT 960  
 Qy 961 ACCAAGTAGCTGAATCCCATTTCTACGCCCTTTCTTGATGAAAACTTCAAGCGGT 1020  
 Db 961 ACCAAGTAGCTGAATCCCATTTCTACGCCCTTTCTTGATGAAAACTTCAAGCGGT 1020  
 Qy 1021 TTCCGGGACTTCTGCTTTTCCACTGAAGATGAGGATGAGCGGAGAGCACTAGCAGAGTC 1080  
 Db 1021 TTCCGGGACTTCTGCTTTTCCACTGAAGATGAGGATGAGCGGAGAGCACTAGCAGAGTC 1080  
 Qy 1081 CGAAATACAGTTACAGGATCTCTTACCTGAGGACATCGATGGATGAATAAACCACTA 1140  
 Db 1081 CGAAATACAGTTACAGGATCTCTTACCTGAGGACATCGATGGATGAATAAACCACTA 1140  
 Qy 1141 TGA 1143  
 Db 1141 TGA 1143  
 RESULT 6  
 US-09-341-446B-5  
 ; Sequence 5, Application US/09341446B  
 ; Patent No. 6518480  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Konklin, Bruce R.  
 ; TITLE OF INVENTION: Selective Target Cell Activation By  
 ; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated  
 ; FILE REFERENCE: Superiorly By Synthetic Ligand  
 ; FILE REFERENCE: UCAL-049CIP  
 ; CURRENT APPLICATION NUMBER: US/09/341,446B  
 ; CURRENT FILING DATE: 1999-12-20  
 ; PRIOR APPLICATION NUMBER: PCT/US97/05334  
 ; PRIOR FILING DATE: 1997-03-25  
 ; PRIOR APPLICATION NUMBER: US 08/622,348  
 ; PRIOR FILING DATE: 1996-03-26  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 5  
 ; LENGTH: 1275  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: RASL OR1  
 US-09-341-446B-5  
 Query Match 86.6%; Score 999.4; DB 4; Length 1275;  
 Best Local Similarity 93.0%; Pred. No. 2e-238;  
 Matches 1061; Conservative 0; Mismatches 71; Indels 9; Gaps 1;  
 Qy 2 TGGACTCCCGATCCAGATCTTCCGCGGGGAGCGGCGGCGGCGGCGGCGGCGGCGGCT 61  
 Db 113 TCGACTCCCGATCCAGATCTTCCGCGGGGAGCGGCGGCGGCGGCGGCGGCGGCGGCT 172

QY 62 GCGTGGCCCGCCAAACAGCAGCGGCTGGTTCCGGGCTGGCCGAGCCGACAGCAACGGCA 121  
 DB 173 GCGTGGCCCGCCAAACAGCAGCGGCTGGTTCCGGGCTGGCCGAGCCGACAGCAACGGCA 232  
 QY 122 GCGCGGCTCGGAGGACGCGAGCTGGAGCCGCGCACATCTCCCGGCGCATCCCGGTCA 181  
 DB 233 GCGCGGCTCGGAGGACGCGAGCTGGAGCCGCGCACATCTCCCGGCGCATCCCGGTCA 292  
 QY 182 TCATCAGCGGCTACTCCGTAGTGTTCGTGGGCTGGTGGGCAATCGCTGGTCA 241  
 DB 293 TCATCAGCGGCTACTCCGTAGTGTTCGTGGGCTGGTGGGCAATCGCTGGTCA 352  
 QY 242 TGTTCGTGATCATCCGATACACAAAGATGAGAGCAGCAACCAATTTACATATTAACC 301  
 DB 353 TGTTCGTGATCATCCGATACACAAAGATGAGAGCAGCAACCAATTTACATATTAACC 412  
 QY 302 TGGCTTTGGCAGATGCTTTAGTTACTACAAACATGCGCTTCAGAGTAGCGTCTACTTCA 361  
 DB 413 TGGCTTTGGCAGATGCTTTAGTTACTACAAACATGCGCTTCAGAGTAGCGTCTACTTCA 472  
 QY 362 TGAATTCCTGGCCTTTTGGGATGCTGTGCAAGATAGTAATTTCCATTGATTACTACA 421  
 DB 473 TGAATTCCTGGCCTTTTGGGATGCTGTGCAAGATAGTAATTTCCATTGATTACTACA 532  
 QY 422 ACATGTTCCAGCATCTTCCTGAGTGTGAGCGTGGACCGCTACATTCGCGTCT 481  
 DB 533 ACATGTTCCAGCATCTTCCTGAGTGTGAGCGTGGACCGCTACATTCGCGTCT 592  
 QY 482 GCCACCCCGTGAAGCTTTGGCTTCGCGACACCCCTTGAAGCAAGATCATCAATCT 541  
 DB 593 GCCACCCCGTGAAGCTTTGGCTTCGCGACACCCCTTGAAGCAAGATCATCAATCT 652  
 QY 542 GCATCTGGGTGCTGTGCTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGACCAAG 601  
 DB 653 GCATCTGGGTGCTGTGCTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGACCAAG 712  
 QY 602 TCAGGGAAGACGTCGATGTCATTGAGTGCCTTTCGAGTTCACAGATGATGACTCTCT 661  
 DB 713 CCAGGATGAGCAGTGATGACGCTCAGTTCGCCAGCCC-----CAGTGT 763  
 QY 662 GGTGGGACCTCTTCATGAAGATCTGGGTCTTCATCTTTGGCTTCGTGATCCCTGTCTCA 721  
 DB 764 ACTGGGACACTGTGACCAAGATCTGCGTCTTCATCTTTGGCTTCGTGATCCCTGTCTCA 823  
 QY 722 TCATCATCTGCTGTACACCTGATGATCTGGGTCTCAGAGGCTCCGCTCTCTTCTG 781  
 DB 824 TCATCATCTGCTGTACACCTGATGATCTGGGTCTCAGAGGCTCCGCTCTCTTCTG 883  
 QY 782 GCTCCGAGAAAGATCGCAACCTGCTAGGATCACAGACTGGTCTCGTGGTGGTGG 841  
 DB 884 GCTCCGAGAAAGATCGCAACCTGCTAGGATCACAGACTGGTCTCGTGGTGGTGG 943  
 QY 842 CAGTCTTGGTGTCTGTGATCCCAATTCATATTCATCTTGGTGGAGGCTCTGGGA 901  
 DB 944 CAGTCTTGGTGTCTGTGATCCCAATTCATATTCATCTTGGTGGAGGCTCTGGGA 1003  
 QY 902 GCACCTCCACAGCAGCTGCTCTCCAGCTATTACTTCTGATCGCTTAGGCTATA 961  
 DB 1004 GCACCTCCACAGCAGCTGCTCTCCAGCTATTACTTCTGATCGCTTAGGCTATA 1063  
 QY 962 CCAACAGTAGCTGAATCCCAATCTCTACGCTTTCTTGATGAATACTTCAAGCGGTGT 1021  
 DB 1064 CCAACAGTAGCTGAATCCCAATCTCTAGGCTTTCTTGATGAATACTTCAAGCGGTGT 1123  
 QY 1022 TCCGGGACTTCTGCTTTCCATGAAGATGAGGATGGAGCGGACAGCACTAGCAGATCC 1081  
 DB 1124 TCCGGGACTTCTGCTTTCCATGAAGATGAGGATGGAGCGGACAGCACTAGCAGATCC 1183  
 QY 1082 GAATACAGTTTCAAGTCTCTCTTACCTGAGGACATCGATGGGATGAATAAACCAGTAT 1141  
 DB 1184 GAATACAGTTTCAAGTCTCTCTTACCTGAGGACATCGATGGGATGAATAAACCAGTAT 1243  
 QY 1142 G 1142

DB 1244 G 1244

RESULT 7

US-09-341-446B-7  
 ; Sequence 7, Application US/09341446B  
 ; Patent No. 6518480  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Conklin, Bruce R.  
 ; TITLE OF INVENTION: Selective Target Cell Activation By  
 ; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated  
 ; TITLE OF INVENTION: Superiorly By Synthetic Ligand  
 ; FILE REFERENCE: UCAL-049CIP  
 ; CURRENT APPLICATION NUMBER: US/09/341,446B  
 ; CURRENT FILING DATE: 1999-12-20  
 ; PRIOR APPLICATION NUMBER: PCT/US97/05334  
 ; PRIOR FILING DATE: 1997-03-25  
 ; PRIOR APPLICATION NUMBER: US 08/622,348  
 ; PRIOR FILING DATE: 1996-03-26  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 7  
 ; LENGTH: 1275  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: RASL OR2  
 US-09-341-446B-7

Query Match 86.2%; Score 994.6; DB 4; Length 1275;  
 Best Local Similarity 92.7%; Pred. No. 3e-237;  
 Matches 1058; Conservative 0; Mismatches 74; Indels 9; Gaps 1;  
 QY 2 TGGACTCCCGATCAGATCTTCGCGGGGAGCGCGGCTTACCTGCGCCCGAGCGCT 61  
 DB 113 TCGACTCCCGATCAGATCTTCGCGGGGAGCGCGGCTTACCTGCGCCCGAGCGCT 172  
 QY 62 GCGTGGCCCGCCAAACAGCAGCGCTGGTTTCCGGCTGGGCGGAGCCGACAGCAACGGCA 121  
 DB 173 GCGTGGCCCGCCAAACAGCAGCGCTGGTTTCCGGCTGGGCGGAGCCGACAGCAACGGCA 232  
 QY 122 GCGCGGCTCGAGGACGCGGAGCTGGAGCCGCGCACATCTCCCGGCGCATCCCGGTCA 181  
 DB 233 GCGCGGCTCGAGGACGCGGAGCTGGAGCCGCGCACATCTCCCGGCGCATCCCGGTCA 292  
 QY 182 TCATCAGCGGCTTACTCCGTAGTGTTCGTGGGCTGGTGGGCAACTCGCTGGTCA 241  
 DB 293 TCATCAGCGGCTTACTCCGTAGTGTTCGTGGGCTGGTGGGCAACTCGCTGGTCA 352  
 QY 242 TGTTCGTGATCATCCGATACACAAAGATGAGAGCAGCAACCAATTTACATATTAACC 301  
 DB 353 TGTTCGTGATCATCCGATACACAAAGATGAGAGCAGCAACCAATTTACATATTAACC 412  
 QY 302 TGGCTTTGGCAGATGCTTTAGTTACTACAAACATGCGCTTCAGAGTAGCGTCTACTTCA 361  
 DB 413 TGGCTTTGGCAGATGCTTTAGTTACTACAAACATGCGCTTCAGAGTAGCGTCTACTTCA 472  
 QY 362 TGAATTCCTGGCCTTTTGGGATGCTGTGCAAGATAGTAATTTCCATTGATTACTACA 421  
 DB 473 TGAATTCCTGGCCTTTTGGGATGCTGTGCAAGATAGTAATTTCCATTGATTACTACA 532  
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 DB 533 ACATGTTCCAGCATCTTCCTGAGTGTGAGCGTGGACCGCTACATTCGCGTCT 592  
 QY 482 GCCACCCCGTGAAGCTTTGGCTTCGCGACACCCCTTGAAGCAAGATCATCAATCT 541  
 DB 593 GCCACCCCGTGAAGCTTTGGCTTCGCGACACCCCTTGAAGCAAGATCATCAATCT 652  
 QY 542 GCATCTGGGTGCTGTGCTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGACCAAG 601  
 DB 653 GCATCTGGGTGCTGTGCTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGACCAAG 712

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Qy 602 TCAGGGAAGACGTGATGCTATGAGTCTCTCTTGCAGTTCCTCCAGATGATGACTACTCCT 661
Db 713 CCGGGATGGAGCAGTGTGATGACGCTCCAGTTCCTCCAGGCC-----CAGTGGT 763
Qy 662 GGTGGGACCTCTTCAATGAAGATCTGCGTCTTCACTTTGCTTGGCTTGTGATCTCTGCTCTCA 721
Db 764 ACTGGGACACTGTGACCAAGATCTGCGTCTTCACTTTGCTTGTGATCTCTGCTCTCA 823
Qy 722 TCATCATCTGTCTGTACACCTCTGATGATCTCTGCGTCTCAAGAGCGTCCGGCTCTCTTCTG 781
Db 824 TCATCATCTGTCTGTACACCTCTGATGATCTCTGCGTCTCAAGAGCGTCCGGCTCTCTTCTG 883
Qy 782 GCTCCGAGAGAAAGATCGCAACCTGCTAGATGATCTCTGCGTCTCAAGAGCGTCCGGCTCTG 841
Db 884 GCTCCGAGAGAAAGATCGCAACCTGCTAGATGATCTCTGCGTCTCAAGAGCGTCCGGCTCTG 943
Qy 842 CAGTCTTCTGTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 901
Db 944 CAGTCTTCTGTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1003
Qy 902 GCACCTCCACAGACAGCTGCTCTCTCCAGCTATTACTTCTGATCGCTTACGCTATA 961
Db 1004 GCACCTCCACAGACAGCTGCTCTCTCCAGCTATTACTTCTGATCGCTTACGCTATA 1063
Qy 962 CCAACAGTAGCTGAATCCCACTTCTACGCTTCTTGTGATGAAACTTCAAGCGGTGT 1021
Db 1064 CCAACAGTAGCTGAATCCCACTTCTACGCTTCTTGTGATGAAACTTCAAGCGGTGT 1123
Qy 1022 TCCGGGACTTCTGCTTCCACCTGAGATGAGATGAGGAGCGGCGAGCACTAGCAGTCC 1081
Db 1124 TCCGGGACTTCTGCTTCCACCTGAGATGAGATGAGGAGCGGCGAGCACTAGCAGTCC 1183
Qy 1082 GAAATACAGTTCAGGATCTGCTTACCTGAGGACATCGATGGGATGAATAAACAGTAT 1141
Db 1184 GAAATACAGTTCAGGATCTGCTTACCTGAGGACATCGATGGGATGAATAAACAGTAT 1243
Qy 1142 G 1142
Db 1244 G 1244

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# RESULT 8

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US-09-214-904-5
; Sequence 5, Application US/09214904
; Patent No. 6632977
; GENERAL INFORMATION:
; APPLICANT: TRANSGENIC ANIMAL IN WHICH THE EXPRESSION
; TITLE OF INVENTION: OF OPIATE RECEPTORS IS MODIFIED
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/214,904
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR97/01282
; FILING DATE:
; APPLICATION NUMBER: FR 96.08810
; FILING DATE: 15-JUL-1996
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1408 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS

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LOCATION: 184..1323  
US-09-214-904-5

Query Match	78.8%	Score	909.2	DB 4	Length	1408
Best Local Similarity	86.7%	Pred. No.	5.2e-216	Mismatches	0	Gaps
Matches 1001	Conservative	0				

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Db 184 ATGGAGTCCCCCAATTCAGATCTTCCGAGGAGATCCAGGCCCTACTGTCTCTCCAGTGCT 243
Qy 61 TGCCTGCCCCCAACAGCAGCGGCTGTGTTTCCCGGCTGGGCGGAGCCCGACAGACACGGC 120
Db 244 TGCCTTCTCCCAACAGCAGCGCTCTTGGTTCCCAACTGGGCGAGAAATCCGACAGTAATGGC 303
Qy 121 AGCCCGCGCTCGAGGAGCGGACGTGAGCGCCGCGACATCTCCCGGCCCATCCCGGTC 180
Db 304 AGTGTGGGCTCAGAGGATCAGCAGCTGAGTCCGCGACATCTCTCCGCCCATCCCTGTT 363
Qy 181 ATCATCAGCGGCTACTCTCGTAGTGTCTCGTGGGCTTTGGTGGGCAACTCGCTGGTC 240
Db 364 ATCATCAGCGCTACTCTGTGTATTTGTGGTGGGCTTTAGTGGGCAATCTCTCTGGTC 423
Qy 241 ATGTTCTGTATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTATATTAAAC 300
Db 424 ATGTTCTGTATCATCCGATACACAAAGATGAAGACCGCAACCAACATCTCATATTAAAC 483
Qy 301 CTGCTTTTGGCAGATGCTTTAGTTACTACCAACCATGCCCTTTTCAAGTACGCTCTACTTG 360
Db 484 CTGCTTTTGGCAGATGCTTTAGTTACTACCAACCATGCCCTTTTCAAGTACGCTCTACTTG 543
Qy 361 ATGAATTTCTGGGCTTTTGGGATGTCTGTGCAAGATAGTAATTTCCATTGATTACTTAC 420
Db 544 ATGAATTTCTGGGCTTTTGGGATGTCTGTGCAAGATAGTAATTTCCATTGATTACTTAC 603
Qy 421 AACATGTTTACCAGATCTTCACTTGAACCATGAGCGTGGACCGGTACATTGCGCGTG 480
Db 604 AACATGTTTACCAGATCTTCACTTGAACCATGAGCGTGGACCGGTACATTGCGCGTG 663
Qy 481 TGCCACCCCGTGAAGGCTTTGGAGCTTCCGACACCCCTTGAAGGCAAGATCATCAATATC 540
Db 664 TGCCACCCCGTGAAGGCTTTGGAGCTTCCGACACCCCTTGAAGGCAAGATCATCAATATC 723
Qy 541 TGATCTGGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 600
Db 724 TGATTTGGTCTCTGGCATCATCTGTTGGTATATACGGATAGTCTTGGAGGACCAAA 783
Qy 601 GTGAGGAAGACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Db 784 GTGAGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 843
Qy 661 TGTGGGACCTCTTCAATGAAGATCTGCTTCACTTTTGGCTTCTGTGATCCCTGTCTCTC 720
Db 844 TGTGGGATCTTCTCATGAAGATCTGCTTCTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTT 903
Qy 721 ATCATCATCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 780
Db 904 ATCATCATCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 963
Qy 781 GGCTCCCGAGAGAAAGATCGCAACCTCGTAGGATACACAGACTGGTCTGGTGGTGGTG 840
Db 964 GGCTCCCGAGAGAAAGATCGCAACCTCGTAGGATACACAGACTGGTCTGGTGGTGGTG 1023
Qy 841 GCAGTCTTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 900
Db 1024 GCAGTCTTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 1083
Qy 901 AGCACTCTCCACAGCAGCTGTCTCTCCAGCTATTACTTCTGCATCGCTTACGGCTAT 960
Db 1084 AGCACTCTCCACAGCAGCTGTCTCTCCAGCTATTACTTCTGCATCGCTTACGGCTAT 1143
Qy 961 ACCAAGATAGCTGAATCCCACTTCTCTAGCGCTTCTTGTATGAAACTTCAACGGGTGT 1020

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Db 1144 ACCAACAGCAGCCTGAATCTGTTCTCTATGCTTTCTGATGAAATCTCAAGCGGTG 1203  
 QY 1021 TTCCGGGACTTGTCTTTTCCACTGAAGATGAGGATCGAGCGGAGAGCTAGCAGAGTC 1080  
 Db 1204 TTATAGGACTTCTGCTTCCCTATTAAAGATGCGAATGGAGCGCCAGAGCACCAGT 1263  
 QY 1081 CGAAATACAGTTCAGGATCTGCTTACCTGAGGACATCGATGGGATGAATAACAGTA 1140  
 Db 1264 AGAAACACAGTTCAGGATCTGCTTCCATGAGAGATGTGGGAGGATGAATAAGCCAGTA 1323  
 QY 1141 TGAAGTCTGTGGA 1154  
 Db 1324 TGAAGTCTGTGGA 1337

RESULT 9

US-08-147-592A-1  
 ; Sequence 1, Application US/08147592A  
 ; Patent No. 6096513  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bell, Graeme I  
 ; APPLICANT: Reisine, Terry  
 ; APPLICANT: Yasuda, Kazuki  
 ; TITLE OF INVENTION: Opioid Receptor Genes,  
 ; TITLE OF INVENTION: Compositions and Methods  
 ; NUMBER OF SEQUENCES: 43  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Arnold, White & Durkee  
 ; STREET: P.O. Box 4433  
 ; CITY: Houston  
 ; STATE: Texas  
 ; COUNTRY: United States of America  
 ; ZIP: 72210  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/147,592A  
 ; FILING DATE: 05-NOV-1993  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/100,694  
 ; FILING DATE: 30-JUL-1993  
 ; CLASSIFICATION: 435  
 ; APPLICATION NUMBER: 08/066,296  
 ; FILING DATE: 20-MAY-1993  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Wilson, Mark B.  
 ; REGISTRATION NUMBER: 37,259  
 ; REFERENCE/DOCKET NUMBER: ARCD:105  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (512) 418-3000  
 ; TELEFAX: (512) 474-7577  
 ; TELEX: N/A  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1410 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 186..1325  
 ; US-08-147-592A-1

Query Match 78.8%; Score 909.2; DB 3; Length 1410;  
 Best Local Similarity 86.7%; Pred. No. 5.2e-216;  
 Matches 1001; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

QY 1 ATGGAATCCCGATCCAGATCTTCCGCGGGAGCGGGCCCTTACCTGCGCGCCGAGCGCC 60  
 Db 186 ATGGAATCCCGATCCAGATCTTCCGAGAGATCCAGGCCCTACCTGCTCTCCAGTGT 245  
 QY 61 TGCCTGCCCGCCAAACAGCAGCGCTGTGTTCCGCGCTGGGCGGAGCCCGACAGCAAGCGC 120  
 Db 246 TGCCTTCTCCCGCCAAACAGCAGCTTGTGTTCCCGAACCTGGGCGAGATCCGACAGTAATGCG 305  
 QY 121 AGCGCGGCTCGGAGGACGCGCAGCTGAGCGCGGACATCTCCCGGCGCATCCCGGTTC 180  
 Db 306 AGTGTGGGCTCAGAGGATCAGCAGCTGGAGTCCGCGCACATCTCTCCGCGCATCCCTGTT 365  
 QY 181 ATCATCAGCGGCTTACTCTCGTGTGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 240  
 Db 366 ATCATCAGCGGCTTACTCTCTGTGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 425  
 QY 241 ATGTTCTGTGATCATCCGATACAAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300  
 Db 426 ATGTTTGTGATCATCCGATACAAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 485  
 QY 301 CTGGCTTTGGCAGATGCTTTAGTTACTACCAATGCTTCTTACAGAGTACGCTTCTACTTG 360  
 Db 486 CTGGCTTTGGCAGATGCTTTAGTTACTACCAATGCTTCTTACAGAGTACGCTTCTACTTG 545  
 QY 361 ATGAATTTCTGGGCTTTTGGGATGCTGTGTCAGAGATAGTAATTTCCATTTGATTTACTAC 420  
 Db 546 ATGAATTTCTGGGCTTTTGGGATGCTGTGTCAGAGATAGTAATTTCCATTTGATTTACTAC 605  
 QY 421 AACATGTTTACAGCATCTTCACTTACCATGATGAGGTGGAGCGGTACATTTCCCGCTG 480  
 Db 606 AACATGTTTACAGCATCTTCACTTACCATGATGAGGTGGAGCGGTACATTTCCCGCTG 665  
 QY 481 TGCCACCCCGTGAAGGCTTTTGGACTTCCGACACACCTTTGAAGGCAAGATCATCAATATC 540  
 Db 666 TGCCACCCCGTGAAGGCTTTTGGACTTCCGACACACCTTTGAAGGCAAGATCATCAATATC 725  
 QY 541 TGCAATCTGGCTGCTGTGCTGATGCTGCTGATGCTGCTGATGCTGCTGATGCTGCTGCTGCT 600  
 Db 726 TGCAATCTGGCTGCTGTGCTGATGCTGCTGATGCTGCTGATGCTGCTGATGCTGCTGCTGCT 785  
 QY 601 GTCCAGGAGAGTGTGATGCTGCTGATGCTGCTGATGCTGCTGATGCTGCTGATGCTGCTGCT 660  
 Db 786 GTCCAGGAGAGTGTGATGCTGCTGATGCTGCTGATGCTGCTGATGCTGCTGATGCTGCTGCT 845  
 QY 661 TGTGGGAGCTCTTCAATGAAGATCTGCGTCTTCACTTGTGCTTGTGCTTGTGCTTGTGCTTGT 720  
 Db 846 TGTGGGAGCTCTTCAATGAAGATCTGCTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGT 905  
 QY 721 ATCATCATCTGCTGCTTACACCTGATGATCTGCGGTCTCAAGAGCGTCCGGCTCCTTTCT 780  
 Db 906 ATCATCATCTGCTGCTTACACCTGATGATCTGCGGTCTCAAGAGTGTCCGGCTCCTTTCT 965  
 QY 781 GGCTCCCGAGAGAGATCGCAACCTGCTAGAGTACCCAGACTGCTGCTGCTGCTGCTGCTGCTG 840  
 Db 966 GGCTCCCGAGAGAGATCGCAACCTGCTAGAGTACCCAGACTGCTGCTGCTGCTGCTGCTGCTG 1025  
 QY 841 GCAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
 Db 1026 GCAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1085  
 QY 901 AGCAGCTCCACAGCAGCAGTGTCTCTCCAGTATTACTTCTGATCCGCTTACGCTTAT 960  
 Db 1086 AGCAGCTCCACAGCAGCAGTGTCTCTCCAGTATTACTTCTGATGCTGCTGCTGCTGCTGCTG 1145  
 QY 961 ACCACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020  
 Db 1146 ACCACAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1205  
 QY 1021 TTCCGGGACTTCTGCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080  
 Db 1206 TTATAGGACTTCTGCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1265  
 QY 1081 CGAAATACAGTTCAGGATCTGCTTACCTGAGGACATCGATGGGATGAATAACAGTA 1140

Db · 1266 AGAAACAGTTTCAGGATTCCTGCTTCATGAGAGATGTGGGAGGGATGAATTAGCCAGTA 1325

QY 1141 TGACTAGTCGTGGA 1154  
Db 1326 TGACTAGTCGTGGA 1339

## RESULT 10

US-08-292-694A-1  
; Sequence 1, Application US/08292694A  
; Patent No. 6319686  
; GENERAL INFORMATION:  
; APPLICANT: BELL, GRAEME  
; APPLICANT: REISINE, TERRY  
; APPLICANT: YASUDA, KAZUKI  
; TITLE OF INVENTION: OPIOID RECEPTORS: COMPOSITIONS AND METHODS

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: COUNTRY: USA
: ZIP: 77210
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
: SOFTWARE: Patent In Release #1.0, Version #1.25

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; ;
; APPLICATION NUMBER: US/08/292,694A
; FILING DATE: August 19, 1994
; CURRENT APPLICATION DATA:

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CLASSIFICATION: 400  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/066,296

CLASSIFICATION: 435  
FILING DATE: 20 MAY 1953  
APPLICATION NUMBER: 08/100,694

CLASSIFICATION: 435  
FILING DATE: 30 JULY, 1993  
APPLICATION NUMBER: 08/147 592

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;
;
; FILING DATE: 5 NO. 6319686emdef 1993
; CLASSIFICATION: 435
; APPLICATION NUMBER: PCT/US94/05747
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CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
FILING DATE: 20 May 1994

NAME: MARK B. WILSON  
REGISTRATION NUMBER: 37,259  
REFERENCE/DOC#ET NUMBER: ADSD-140/WTM

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
FAX: (512) 700-2670

TELEX: 79-0924  
INFORMATION FOR SEQ ID NO: 1

LENGTH: 1410 base pairs  
TYPE: nucleic acid  
COMMENT: CDS: 24-1410

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;
; TOPOLOGY: linear
;
; MOLECULE TYPE: genomic DNA
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; NAME/KEY: CDS
; LOCATION: 186..1325
; .....
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Query Match	Score	DB 3	Length
78.8%	909.2	DB 3	Length 1410

Matches 1001; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

\_\_\_\_\_



NUMBER OF SEQUENCES: 46  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Arnold, White & Durkee  
 STREET: P. O. Box 4433  
 CITY: Houston  
 STATE: Texas  
 COUNTRY: USA  
 ZIP: 77210  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/292.694A  
 FILING DATE: August 19, 1994  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/066,296  
 FILING DATE: 20 May 1993  
 CLASSIFICATION: 435  
 APPLICATION NUMBER: 08/100,694  
 FILING DATE: 30 July, 1993  
 CLASSIFICATION: 435  
 APPLICATION NUMBER: 08/147,592  
 FILING DATE: 5 No. 6319686ember 1993  
 CLASSIFICATION: 435  
 APPLICATION NUMBER: PCT/US94/05747  
 FILING DATE: 20 May 1994  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MARK B. WILSON  
 REGISTRATION NUMBER: 37,259  
 REFERENCE/DOCKET NUMBER: ARCD:140/WIM  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (512) 418-3000  
 TELEFAX: (713) 789-2679  
 TELEX: 79-0924  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1000 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 FEATURE:  
 NAME/KEY: N  
 LOCATION: 607-608, 642-643, 896, 906  
 IDENTIFICATION METHOD: N = A, C, G or T  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 102..986  
 FEATURE:  
 NAME/KEY: Xaa  
 LOCATION: 169, 181, 265, 269  
 IDENTIFICATION METHOD: Xaa = unknown  
 US-08-292-694A-11

Query Match 75.4%; Score 869.6; DB 3; Length 1000;  
 Best Local Similarity 97.5%; Pred. No. 3.1e-206;  
 Matches 891; Conservative 0; Mismatches 20; Indels 3; Gaps 1;  
 Qy 244 TTCCTGATCCGATACACAAAGATGAAGACAGCAACATTTACATATTTAACTG 303  
 Db 87 TCTCTTTCTTTAGATACACAAAGATGAAGACAGCAACATTTACATATTTAACTG 146  
 Qy 304 GCTTTGGCAGATGCTTTAGTTACTACACCAATGCCCTTTACAGTACGGTCTACTTGATG 363  
 Db 147 GCTTTGGCAGATGCTTTAGTTACTACACCAATGCCCTTTACAGTACGGTCTACTTGATG 206  
 Qy 364 AATTCTGGCCCTTTGGGGATGCTGTGCAAGATAGTAATTTCCATGATTACTACAC 423  
 Db 207 AATTCTGGCCCTTTGGGGATGCTGTGCAAGATAGTAATTTCCATGATTACTACAC 266

Qy 424 ATGTTTACCAGCATCTTTACCTTGACCATGATGAGCGTGGAACCGCTACATTGCGGTGTC 483  
 Db 267 ATGTTTACCAGCATCTTTACCTTGACCATGATGAGCGTGGAACCGCTACATTGCGGTGTC 326  
 Qy 484 CACCCCGTGAAGGCTTTGGACTTCGGCACACCCCTTGAAGGCAAAAGATCATCAATATCTGC 543  
 Db 327 CACCCCGTGAAGGCTTTGGACTTCGGCACACCCCTTGAAGGCAAAAGATCATCAATATCTGC 386  
 Qy 544 ATCTGGCTGCTGCTGATCATCTGTTGGCATCTCTCAATAGTCTTGGAGGACCAAAAGTC 603  
 Db 387 ATCTGGCTGCTGCTGATCATCTGTTGGCATCTCTCAATAGTCTTGGAGGACCAAAAGTC 446  
 Qy 604 AGGAAGACGTCGATGTCATTTAGTGTCTTCCAGAGTTCAGATGATGATCTACTCTCTGG 663  
 Db 447 AGGAAGGTCGATGTCATTTAGTGTCTTCCAGATTCAGATGATGATCTACTCTCTGG 506  
 Qy 664 TGGACCTCTTCATGAAGATCTGGCTCTTCACTTTGCTGCTGATGATGATGATGATGATGATG 723  
 Db 507 TGGACCTCTTCATGAAGATCTGGCTCTTCACTTTGCTGCTGATGATGATGATGATGATGATG 566  
 Qy 724 ATCATGCTGCTACACCCCTGATGATCTGCTGCTCAAGAGCGTCCGCTCCTTTCTGTC 783  
 Db 567 ATCATGCTGCTACACCCCTGATGATCTGCTGCTCAAGAGGCTCCGCTCCTTTCTGTC 626  
 Qy 784 TCCGAGAGAAAGATCGCAACCTGCTGATGATCACCAGACTGGTCTCTGGTGGTGGTGGCA 843  
 Db 627 TCCGAGAGAAAGATNNAACCTGCTGATGATCACCAGACTGGTCTCTGGTGGTGGTGGCA 686  
 Qy 844 GTCTTCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 903  
 Db 687 GTCTTCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 746  
 Qy 904 ACCTCCACAGCAGCTGCTCTCCAGCTATTTACTTCTGATGATGATGATGATGATGATGATGATG 963  
 Db 747 ACCTCCACAGCAGCTGCTCTCCAGCTATTTACTTCTGATGATGATGATGATGATGATGATGATG 806  
 Qy 964 AACAGTAGCCTGATCCCATTTCTACGCTCTTCTGATGATGATGATGATGATGATGATGATGATG 1023  
 Db 807 AACAGTAGCCTGATCCCATTTCTACGCTCTTCTGATGATGATGATGATGATGATGATGATGATG 866  
 Qy 1024 CGGACTTCTGCTTCCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1083  
 Db 867 CGGACTTCTGCTTCCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 926  
 Qy 1084 AATACAGTTCAGGATCCTGCTTACCTGAGGACATCGATG- --GATGAATAAACCACTA 1140  
 Db 927 AATACAGTTCAGGATCCTGCTTACCTGAGGAGATCGATGATGATGATGATGATGATGATGATG 986  
 Qy 1141 TGACTAGTCTGGA 1154  
 Db 987 TGACTAGTCTGGA 1000

RESULT 13  
 US-08-430-286A-1  
 ; Sequence 1, Application US/08430286A  
 ; Patent No. 6225080  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Uhl, George R.  
 ; APPLICANT: Eppler, C. Mark  
 ; APPLICANT: Wang, Jai-Bel  
 ; TITLE OF INVENTION: Mu-Subtype Opioid Receptor  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Darby & Darby PC  
 ; STREET: 805 Third Avenue  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: US  
 ; ZIP: 10022  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk

Thu Apr 7 08:55:54 2005

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/430,286A  
FILING DATE: 28-APR-1995  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Robinson, Joseph R.  
REGISTRATION NUMBER: 33,448  
REFERENCE/DOCKET NUMBER: 0646/JA843-US5  
TELEPHONE: 212-527-7700  
TELEFAX: 212-753-6237  
TELEX: 236687  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2135 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
ORIGINAL SOURCE:  
ORGANISM: Rattus rattus  
IMMEDIATE SOURCE:  
CLONE: mu receptor cDNA  
US-08-430-286A-1

Query Match 38.7%; Score 446.4; DB 3; Length 2135;  
Best Local Similarity 66.9%; Pred. No. 5,7e-101;  
Matches 669; Conservative 0; Mismatches 321; Indels 9; Gaps 2;

Qy 110 ACAGCAACGGCAGCGCGCTCGAGAGACGGCAGCTGGAGCGCGGCACATCTCCCGG 169  
Db 167 ACCGACCGGCTGGCGGGAACGACAGCGCTGTGCGCTCAGACCGCGCCCTTCCATGG 226  
Qy 170 CCATCCGGTCAATCATCACCGCGGTCTACTCCGTAGTGTTCGTGGGCTTGGTGGCA 229  
Db 227 TCACAGCCATTACCATCATGGCCCTCTACTCTATGCTGTGTAGTGGGCTTTCGGA 286  
Qy 230 ACTCGCTGATCATGTTCTGCTGATCATCGGATACCAAGATGAAGACAGCAACCAATTT 289  
Db 287 ACTTCCTGGTCATGATGTGATGTTAAGATACACCAAAATGAAGACTGCCACCAATCT 346  
Qy 290 ACATATTAACTGGCTTGGCAGATGCTTTAGTACTACCAACCTGCTTTCAGAGTA 349  
Db 347 ACATTTTCACTTGGCTTGGCAGACGCTTAGGACCACTACCTGCTTTCAGAGTG 406  
Qy 350 CGGCTACTTATGATCAATTCCTGGCTTTTGGGATGTGCTGTGCAAGATAGTAATTTCA 409  
Db 407 TCAACTACCTGATGGGAACATGGCCCTTCGGAACCATCTCTGCAAGATGTGATCTCA 466  
Qy 410 TTGATTACTACACATGTTTCAACAGATCTTCACTTGAACATGATGAGGTGACCGCT 469  
Db 467 TAGATTACTACACATGTTTCAACAGATATTCACCTCTGCAACCATGATGAGGTGACCGCT 526  
Qy 470 ACATGGCGTGGCCACCGGTGAGGCTTGGACTTCCGACACCTTGAAGCAAGA 529  
Db 527 ACATTTGTGTCTGCCACCCAGTCAAGCGCTTGGATTTCCGTACCCCGGAATGCCAAA 586  
Qy 530 TCATCAATATCTGATCTGGCTGTGCTGCTCATCTGTGGCATCTGTGCAATAGTCTTG 589  
Db 587 TCGTCAAGCTTGGCACTGGATCTCTCTCTGCACTGGTCTGCTGTAATGTTCTATGG 646  
Qy 590 GAGGACCAAGTACAGGAAGACGTGATGATGATGATGATGATGATGATGATGATGATG 649  
Db 647 CAACCAAAAATACAGGAGGGGTC-----CATAGATTGACCCCTCAGCTTCTCCACC 700  
Qy 650 ATGACTACTCTTGGTGGACCTCTTCAATGAAGATCTGCTTCTATCTTTTCCCTTCGTA 709  
Db 701 CAACTGGTACTGGAGAACTGTCTC---AAATCTGTGCTTTTATCTTCTGCTTTCA 757  
Qy 710 TCCCTGTCTCATCATCATATGCTGTGCTACACCCCTGATGATCTCTGCTCTCAAGAGCGTCC 769

Db 758 TGGCGGCTCTCATCATCATCTGTGTGTACGGCTGTGATGATCTTACGACTCAAGAGCGTTC 817  
Qy 770 GGCTCCCTTTCTGGCTCCCGAGAGAAAGATCGAACCTCGGTAGGATCACCAGACTGGTCC 829  
Db 818 GCATGCTATCGGGCTCCAAAAGAAAGACAGGAATCTGCGCAGGATCACCAGGATGTCG 877  
Qy 830 TGGTGGTGGGAGTCTTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 889  
Db 878 TGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 937  
Qy 890 AGGCTCTGGGAGACACCTCCACAGCAGCAGTGTCTCTCCAGGTATATCTTCTGCTG 949  
Db 938 AAGCGCTGATCAGGATTCAGAAACACATTTCCAGACCGTTCCTGGCAGCTTCTGCTG 997  
Qy 950 CTTAGGCTATACCAACAGTAGCTGATCCCATCTCTAGCGCTTCTTGTGATGAAACT 1009  
Db 998 CTTTGGGTTACAGAACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1057  
Qy 1010 TCAAGCGGTGTTCCGGGACTTCTGCTTCCACTGAAGATGAGGATGAGCGGAGAGCA 1069  
Db 1058 TCAAGCGATGCTTACAGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1117  
Qy 1070 CTAGCAGAGTCCGAAATACAGTTTCCAGATCTGCTTCTTCTGCTGCTGCTGCTGCT 1107  
Db 1118 CCACTCGAGTCCGTACAGAACACTAGGGAACATCCCTCC 1155

RESULT 14  
US-08-889-108-1  
; Sequence 1, Application US/08889108  
; Patent No. 6103492  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Lei  
; TITLE OF INVENTION: Mu Opioid Receptors: Compositions and Methods  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Arnold, White & Durkee  
; STREET: P. O. Box 4433  
; CITY: Houston  
; STATE: TX  
; COUNTRY: USA  
; ZIP: 77210-4433  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/889,108  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/305,518  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wilson, Mark B.  
; REGISTRATION NUMBER: 37,259  
; REFERENCE/DOCKET NUMBER: INDA005\WIM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 512-418-3000  
; TELEFAX: 512-474-7577  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1618 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (cdna)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 214..1410  
; US-08-889-108-1

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RESULT 15
US-08-889-108-3
; Sequence 3, Application US/08889108
; Patent No. 6103492
; GENERAL INFORMATION:
; APPLICANT: Yu, Lei
; TITLE OF INVENTION: Mu Opioid Receptors: Compositions and Methods
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/889,108
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/305,518
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: INDA005\WIM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1618 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (cdna)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 339..1235
; US-08-889-108-3

Query Match 38.5%; Score 444.8; DB 3; Length 1618;
Best Local Similarity 66.8%; Pred. No. 1.3e-100;
Matches 667; Conservative 0; Mismatches 322; Indels 9; Gaps 2;

Qy 110 ACAGCAACGCGACGCGCGTCTCGAGGAGACGCGCAGCTGGAGCGCCGCGCAATCTCCCGG 169
Db 350 ACCGCAACGCGCTTGGCGGAAACGACGCGCTGTGCCCTCAGACGCGGAGCCCTTCCATGG 409
Qy 170 CCATCCGGTTCATCATCAGCGCGGTCTACTCCGTAGTGTTCGTCTGGGCTTGGTGCGCA 229
Db 410 TCACAGCCATTACCATCATGCGCCCTCTACTCTATCGTGTGTGTAGTGGGCTCTTCGGAA 469
Qy 230 ACTCGTGTGTCTATGTTCTGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTT 289
Db 470 ACTTCTGTGTGATGTATGTGATTGAAGATACACCAAAATGAAGACTGCCACCAACATCT 529
Qy 290 ACATATTAACTGGCTTTGGAGATGCTTTAGTTACTACAAACAATGCCCTTTTCAGAGTA 349
Db 530 ACATTTTCAACCTTGCTCTGGCAGACGCGCTTAGCGACCACTACACTGCCCTTTTCAGAGT 589
Qy 350 CGGTCTACTTGTATGAATTCCTGCGCTTTTCGGGATGTGCTGTGCAAGATAGTAATTTCCA 409
Db 590 TCAACTACCTGATGGGAACATGCGCCCTTCGGAACCATCCTCTGCAAGATCGTGTCTCAA 649
Qy 410 TTGATTACTACACATGTTCCACGAGCATCTTCACCTTTGACCATGATGAGCGTGGACCGCT 469

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Db 650 TAGATTACTAACACATGTTTACCCAGCATATTCACCCCTCTGCACCATGAGCGTGGACCGCT 709  
QY 470 ACATTGCGGTGTGCGACCCCGTGAAGGCTTTGGACTTTCCGCACACCCCTTGAAGGCAAGA 529  
Db 710 ACATTGCTGTGCGACCCAGTCAAGCCCTGGATTTCGGTACCCCGGAAATGCCAAA 769  
QY 530 TCATCAATATCTGCATCTGGCTGCTGCTCATCTGTGGCATCTCTGCAATAGTCTCTTG 589  
Db 770 TCGTCAACGCTGCACTGATCTCTCTTTCGCCATCGTCTGCTGTAATGTTTCATGG 829  
QY 590 GAGGACCAAGTCAAGGAGAGCGTCAATGTCATTTAGTGTCTCTTGGCAGTTCCTCCAGATG 649  
Db 830 CAACCACAAAATACAGGCGAGGGTC-----CATAGATTGCACCCCTCACGTTCTCCACC 883  
QY 650 ATGACTACTCCTGGTGGGACCTTCTCATGAAGATCTGCGTCTTCATCTTTGGCTTCGTGA 709  
Db 884 CAACTTGGTACTGGGAGAACCTGCTC---AAATCTGTGTCTTTATCTTCGGCTTTTCATCA 940  
QY 710 TCCTGTCTCTCATCATCTGCTGCTGTACACCCCTGATGATCTCTGCGTCTCAAGAGCGTCC 769  
Db 941 TGCGGATCTCTCATCATCTGCTGTGTACGGCTGATGATCTTACGACTCAAGAGCGTTC 1000  
QY 770 GGCTCCTTTCTGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACAGACTGGTCC 829  
Db 1001 GCATGCTATCGGGCTCCAAAGAAAGAGCAGGAAATCTGGCGAGGATCACCCCGGATGGTGC 1060  
QY 830 TGGTGGTGTGGCAGTCTTTCGTGTCTGCTGGAATCCCATTCACATATTCATCTCGGTGG 889  
Db 1061 TGGTGGTGTGGTGTATTTATCTGCTGTGGACCCCATCCACATCTAGTCATCATCA 1120  
QY 890 AGGCTCTGGGGAGCACCTCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCATCG 949  
Db 1121 AAGCGCTGATCAGGATCCAGAAACACATTTACAGACCGTTTCTGGCATTCTGCATTG 1180  
QY 950 CTTAGGCTATACCAACAGTAGCTGAATCCCAATCTCTACGCTTTCTTGTGATAAACT 1009  
Db 1181 CTTTGGGTTACAGCAACAGCTGCTGAATCCAGTCTTTTACGCTTTCTCTGGATGAAACT 1240  
QY 1010 TCAAGCGGTGTTTCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGCGCAGCA 1069  
Db 1241 TCAAGCGATGCTTTCAGAGAGTCTGATCCCAACCTCGTCCAGATCGAAACAGCAAACT 1300  
QY 1070 CTAGCAGAGTCCGAAATACAGTTTCAGGATCCTGCTTAC 1107  
Db 1301 CCACTCGAGTCCGTCAGAACACTAGGGAACATCCCTCC 1338

Search completed: April 6, 2005, 12:39:38  
Job time : 218 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 6, 2005, 12:28:42 ; Search time 766.333 Seconds  
(without alignments)  
9125.590 Million cell updates/sec

Title: US-09-904-584-2  
Perfect score: 1154  
Sequence: 1 atggactcccgatccagat.....ccagatgactagctgtgga 1154

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5615251 seqs, 3030001701 residues

Total number of hits satisfying chosen parameters: 11230502

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications NA:  
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8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*  
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10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*  
13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*  
14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*  
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21: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*  
22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1154	100.0	1154	11	US-09-904-584-2
2	1152.4	99.9	1154	11	US-09-904-584-1
3	1152.4	99.9	1602	19	US-10-278-698-45
4	1152.4	99.9	1602	19	US-10-278-698-559
5	1150.8	99.7	1154	11	US-09-904-584-3
6	1150.8	99.7	1154	11	US-09-904-584-4
7	1150.8	99.7	1154	11	US-09-904-584-5
8	1150.8	99.7	1154	11	US-09-904-584-6
9	1150.8	99.7	1154	11	US-09-904-584-7
10	1144.4	99.2	1182	15	US-10-225-567A-147
11	1144.4	99.2	1182	15	US-10-345-680-19

12	1144.4	99.2	1182	17	US-10-305-720-1417	Sequence 1417, Ap
13	1144.4	99.2	1182	18	US-10-283-975A-80	Sequence 80, Appl
14	1141.4	98.9	1143	16	US-10-318-661-1	Sequence 1, Appli
15	1136.2	98.5	1284	16	US-10-318-661-3	Sequence 3, Appli
16	1133.4	98.2	1143	15	US-10-345-680-21	Sequence 21, Appl
17	1130.2	97.9	1143	10	US-09-826-509-542	Sequence 542, App
18	1130.2	97.9	1143	19	US-10-925-095-542	Sequence 542, App
19	999.4	86.6	1275	16	US-10-318-661-5	Sequence 5, Appli
20	994.6	86.2	1275	16	US-10-318-661-7	Sequence 7, Appli
21	979.4	84.9	1875	16	US-10-318-661-13	Sequence 13, Appli
22	963.4	83.5	1875	16	US-10-318-661-15	Sequence 15, Appl
23	909.2	78.8	1408	9	US-09-214-904-5	Sequence 5, Appli
24	877.8	76.1	1911	16	US-10-318-661-17	Sequence 17, Appl
C 25	469	40.6	585	13	US-10-027-632-188121	Sequence 188121,
C 26	469	40.6	585	13	US-10-027-632-188122	Sequence 188122,
C 27	469	40.6	585	17	US-10-027-632-188121	Sequence 188121,
C 28	469	40.6	585	17	US-10-027-632-188122	Sequence 188122,
29	444.8	38.5	1618	10	US-09-841-720-1	Sequence 1, Appli
30	444.8	38.5	1618	10	US-09-841-720-3	Sequence 3, Appli
31	434.6	37.7	1464	14	US-10-185-083-25	Sequence 25, Appl
32	434.2	37.6	2951	14	US-10-185-083-21	Sequence 21, Appl
33	434	37.6	1332	14	US-10-185-083-22	Sequence 22, Appl
34	434	37.6	1334	9	US-09-761-962-3	Sequence 3, Appli
35	434	37.6	1334	15	US-10-283-300-3	Sequence 3, Appli
36	434	37.6	1365	9	US-09-761-962-11	Sequence 11, Appl
37	434	37.6	1365	15	US-10-283-300-11	Sequence 11, Appl
38	434	37.6	1373	14	US-10-185-083-51	Sequence 51, Appl
39	434	37.6	1423	9	US-09-761-962-1	Sequence 1, Appli
40	434	37.6	1423	15	US-10-283-300-1	Sequence 1, Appli
41	434	37.6	1440	14	US-10-185-083-15	Sequence 15, Appl
42	434	37.6	1569	14	US-10-185-083-17	Sequence 17, Appl
43	434	37.6	1610	9	US-09-761-962-16	Sequence 16, Appl
44	434	37.6	1610	15	US-10-283-300-16	Sequence 16, Appl
45	434	37.6	1614	14	US-10-185-083-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1  
US-09-904-584-2 Application US/09904584  
; Sequence 2, Application US/09904584  
; Publication No. US20040097704A1  
; GENERAL INFORMATION:  
; APPLICANT: Kreek, Mary Jeanne  
; APPLICANT: Yuforov, Vadim  
; APPLICANT: LaForge, Karl Steven  
; TITLE OF INVENTION: Alleles of the Human Kappa Opioid  
; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods Using Said Alleles, and  
; TITLE OF INVENTION: Methods of Treatment Based Thereon  
; FILE REFERENCE: 600-1-285N  
; CURRENT APPLICATION NUMBER: US/09/904,584  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: 60/218,300  
; PRIOR FILING DATE: 2000-07-14  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1154  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-09-904-584-2

Query Match	100.0%	Score 1154;	DB 11;	Length 1154;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1154;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Oy	1	ATGACTCCCGATCCAGATCTTC	CGGGGAGCGGGCCCTACTG	CGCCCCCGAGCGCC 60
Db	1	ATGACTCCCGATCCAGATCTTC	CGGGGAGCGGGCCCTACTG	CGCCCCCGAGCGCC 60
Oy	61	TGCTGCCCCCACAACAGCAGCGCT	TGTTTCCCGGCTGGGCGGAGCGCC	CAGCAACGGC 120



Qy 661 TGGTGGGACCTTTTCATGAAGATCTGCGTCTTTCATCTTTTGGCTTCGTGATCCCTGTCTC 720  
Db 661 TGGTGGGACCTTTTCATGAAGATCTGCGTCTTTCATCTTTTGGCTTCGTGATCCCTGTCTC 720  
Qy 721 ATCATCATCTGCTGTCTACACCTGATGATCTGCGTCTCAAGAGCGTCCGGCTCTTTCT 780  
Db 721 ATCATCATCTGCTGTCTACACCTGATGATCTGCGTCTCAAGAGCGTCCGGCTCTTTCT 780  
Qy 781 GGCTCCCGAGAGAAGATCGCAACTGCGTAGGATCACAGACTGGTCTCGTGGTGGTG 840  
Db 781 GGCTCCCGAGAGAAGATCGCAACTGCGTAGGATCACAGACTGGTCTCGTGGTGGTG 840  
Qy 841 GCAGTCTTCTGCTGTCTGAGCTCCCATTCACATATTCATCTCTGCTGGAGGCTCTGGGG 900  
Db 841 GCAGTCTTCTGCTGTCTGAGCTCCCATTCACATATTCATCTCTGCTGGAGGCTCTGGGG 900  
Qy 901 AGCACTCCACAGCAGCAGCTGCTCTCAGCTATTTACTTCTGATCGCCCTTAGGCTAT 960  
Db 901 AGCACTCCACAGCAGCAGCTGCTCTCAGCTATTTACTTCTGATCGCCCTTAGGCTAT 960  
Qy 961 ACCAAGCTAGCTGAATCCCATCTCTACGCCCTTTCTTGATGAATACTTCAAGCGGTGT 1020  
Db 961 ACCAAGCTAGCTGAATCCCATCTCTACGCCCTTTCTTGATGAATACTTCAAGCGGTGT 1020  
Qy 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGAGCAGCTAGCAGAGTC 1080  
Db 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGAGCAGCTAGCAGAGTC 1080  
Qy 1081 CGAATACAGTTTCAAGATCTGCTTACCTGAGGAGCATCGATGGATGAATAAACCCAGTA 1140  
Db 1081 CGAATACAGTTTCAAGATCTGCTTACCTGAGGAGCATCGATGGATGAATAAACCCAGTA 1140  
Qy 1141 TGACTAGTCGTGGA 1154  
Db 1141 TGACTAGTCGTGGA 1154

RESULT 3

US-10-278-698-45  
; Sequence 45, Application US/10278698  
; Publication No. US20050037344A1  
; GENERAL INFORMATION:  
; APPLICANT: PathoArray GmbH  
; APPLICANT: Stuhlmüller, Bruno  
; APPLICANT: Haupl, Thomas  
; TITLE OF INVENTION: Nucleic Acid Array  
; FILE REFERENCE: 03002705  
; CURRENT APPLICATION NUMBER: US/10/278,698  
; CURRENT FILING DATE: 2002-10-23  
; NUMBER OF SEQ ID NOS: 1050  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 45  
; LENGTH: 1602  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-278-698-45

Query Match 99.9%; Score 1152.4; DB 19; Length 1602;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1153; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 ATGACTCCCCGATCCAGATCTTCGCGGGAGCGGGCCCTACTGCGGCCCGAGCGCC 60  
Db 376 ATGACTCCCCGATCCAGATCTTCGCGGGAGCGGGCCCTACTGCGGCCCGAGCGCC 435  
Qy 61 TGCTGCCCCCAACAGCAGCGCTGTGTTTCCCGCTGGGCGGAGCCCGACAGCAACGGC 120  
Db 436 TGCTGCCCCCAACAGCAGCGCTGTGTTTCCCGCTGGGCGGAGCCCGACAGCAACGGC 495  
Qy 121 AGCGCGGCTCGGAGGAGCGGAGCTGGAGCCCGGACATCTCCCGGGCCATCCCGGTC 180  
Db 496 AGCGCGGCTCGGAGGAGCGGAGCTGGAGCCCGGACATCTCCCGGGCCATCCCGGTC 555

Qy 181 ATCATCAGCGCGGTCTACTCCGTAGTGTTCGTCTGGGCTTGGTGGGCAACTCGCTGGTC 240  
Db 556 ATCATCAGCGCGGTCTACTCCGTAGTGTTCGTCTGGGCTTGGTGGGCAACTCGCTGGTC 615  
Qy 241 ATGTTCTGTGATCATCCGATACACAAAGATGAAGACAGCAACATTTATCATATTTAAAC 300  
Db 616 ATGTTCTGTGATCATCCGATACACAAAGATGAAGACAGCAACATTTATCATATTTAAAC 675  
Qy 301 CTGGCTTTGGCAGATGCTTTTGTAGTTACTACAAACATGCCCTTTCAGAGTACGGTCTACTTG 360  
Db 676 CTGGCTTTGGCAGATGCTTTTGTAGTTACTACAAACATGCCCTTTCAGAGTACGGTCTACTTG 735  
Qy 361 ATGAATTTCTGGCCCTTTTGGGGATGTGCTGTGCAAGATAGTAAATTTCCATTTGATTTACTAC 420  
Db 736 ATGAATTTCTGGCCCTTTTGGGGATGTGCTGTGCAAGATAGTAAATTTCCATTTGATTTACTAC 795  
Qy 421 AACATGTTTCAACAGACTCTTCACTTGAACATGATGAGCGTGGACCGCTACATTTGCCGTG 480  
Db 796 AACATGTTTCAACAGACTCTTCACTTGAACATGATGAGCGTGGACCGCTACATTTGCCGTG 855  
Qy 481 TGCCACCCCGTGAAGGCTTTTGGACTTCCGCACACCCCTTGAAGGCAAAAGATCATCAATATC 540  
Db 856 TGCCACCCCGTGAAGGCTTTTGGACTTCCGCACACCCCTTGAAGGCAAAAGATCATCAATATC 915  
Qy 541 TGCACTCTGGCTGTGCTGTCTGTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGCAACAAA 600  
Db 916 TGCACTCTGGCTGTGCTGTCTGTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGCAACAAA 975  
Qy 601 GTCAAGGAAGACGTCGATGTCATTTGAGTGTCTCTTGGAGTCCAGATGATGATCTCTCC 660  
Db 976 GTCAAGGAAGACGTCGATGTCATTTGAGTGTCTCTTGCAGTTCCTGAGATGATGATCTCTCC 1035  
Qy 661 TGGTGGGACCTTTTCATGAAGATCTGCGTCTTTCATCTTTCGCTTTCGCTGCTCTCC 720  
Db 1036 TGGTGGGACCTTTTCATGAAGATCTGCGTCTTTCATCTTTCGCTTTCGCTGCTCTCC 1095  
Qy 721 ATCATCATCTGCTGTCTACACCTGATGATCTGCGTCTCAAGAGCGTCCGGCTCTCTTTCT 780  
Db 1096 ATCATCATCTGCTGTCTACACCTGATGATCTGCGTCTCAAGAGCGTCCGGCTCTCTTTCT 1155  
Qy 781 GGCTCCCGAGAGAAGATCGCAACTGCGTAGGATCACAGACTGGTCTCTGGTGGTGGTG 840  
Db 1156 GGCTCCCGAGAGAAGATCGCAACTGCGTAGGATCACAGACTGGTCTCTGGTGGTGGTG 1215  
Qy 841 GCAGTCTTCTGCTGCTGCACTCCCATTCACATATTCATCTCTGCTGGAGGCTCTGGGG 900  
Db 1216 GCAGTCTTCTGCTGCTGCACTCCCATTCACATATTCATCTCTGCTGGAGGCTCTGGGG 1275  
Qy 901 AGCACTCCACAGCAGCAGCTGCTCTCTCAGCTATTTACTTCTGCACTCGCCTTAGGCTAT 960  
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Qy 961 ACCAAGCTAGCTGAATCCCATTTCTAGCCCTTTCTTGATGAATACTTCAAGCGGTGT 1020  
Db 1336 ACCAAGCTAGCTGAATCCCATTTCTAGCCCTTTCTTGATGAATACTTCAAGCGGTGT 1395  
Qy 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGAGCAGCAGCTAGCAGAGTC 1080  
Db 1396 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGAGCAGCAGCTAGCAGAGTC 1455  
Qy 1081 CGAATAACAGTTTCAAGGATCTGCTTACTGAGGAGCATCGATGGGATGAATAAACCCAGTA 1140  
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Db 1516 TGACTAGTCGTGGA 1529

RESULT 4  
US-10-278-698-559  
; Sequence 559, Application US/10278698

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; Publication No. US20050037344A1
; GENERAL INFORMATION:
; APPLICANT: PathArray GmbH
; APPLICANT: Stuhlmueller, Bruno
; APPLICANT: Haupl, Thomas
; TITLE OF INVENTION: Nucleic Acid Array
; FILE REFERENCE: 030027US
; CURRENT APPLICATION NUMBER: US/10/278,698
; CURRENT FILING DATE: 2002-10-23
; NUMBER OF SEQ ID NOS: 1050
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 559
; LENGTH: 1602
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-278-698-559

Query Match      99.9%; Score 1152.4; DB 19; Length 1602;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1153; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  ATGGACTCCCGATCCAGATCTTCCGGGGAGCGCGCCCTACCTGCGCCCGCGAGCGCC 60
DB      376  ATGGACTCCCGATCCAGATCTTCCGGGGAGCGCGCCCTACCTGCGCCCGCGAGCGCC 435

QY      61  TGGCTGCCCCCAACAGCAGCGCTGGTTTCCGGCTGGGCGGAGCCCGACAGCAACGGC 120
DB      436  TGGCTGCCCCCAACAGCAGCGCTGGTTTCCGGCTGGGCGGAGCCCGACAGCAACGGC 495

QY      121  AGCCCGGCTCGGAGGAGCGGAGCTGGAGCCCGCGCACATCTCCCGCGCATCCCGGTC 180
DB      496  AGCCCGGCTCGGAGGAGCGGAGCTGGAGCCCGCGCACATCTCCCGCGCATCCCGGTC 555

QY      181  ATCATCATCGGCGTCTACTCCGTAGTGTTCGTGGTGGTGGTGGGCAACTCGCTGGTC 240
DB      556  ATCATCATCGGCGTCTACTCCGTAGTGTTCGTGGTGGTGGTGGGCAACTCGCTGGTC 615

QY      241  ATGTGCTGTATCCGATACACAAATGAGACAGCAGCAACCACTTACATATTAAAC 300
DB      616  ATGTGCTGTATCCGATACACAAATGAGACAGCAGCAACCACTTACATATTAAAC 675

QY      301  CTGCGTTTGGCAGATGCTTTAGTTACTACAAACATGCGCTTTCAGAGTACGGTCTATTG 360
DB      676  CTGCGTTTGGCAGATGCTTTAGTTACTACAAACATGCGCTTTCAGAGTACGGTCTATTG 735

QY      361  ATGAATTCCTGGCTTTTGGGATGTGCTGTGCAAGATAGTAATTCATTTACTATAC 420
DB      736  ATGAATTCCTGGCTTTTGGGATGTGCTGTGCAAGATAGTAATTCATTTACTATAC 795

QY      421  AACATGTTCCAGCATCTTCCATTCACCATGATGAGCGTGGACCGCTACATTTGCCGTG 480
DB      796  AACATGTTCCAGCATCTTCCATTCACCATGATGAGCGTGGACCGCTACATTTGCCGTG 855

QY      481  TGCCACCCCGTGAAGGCTTTGGACTTCGCGCACACCTTTGAAGGCAAGATCATCAATATC 540
DB      856  TGCCACCCCGTGAAGGCTTTGGACTTCGCGCACACCTTTGAAGGCAAGATCATCAATATC 915

QY      541  TGCATCTGGCTGTCTGTCTATCTGTGGATCTCTGCAATAGTCTTGGAGGACCAAAA 600
DB      916  TGCATCTGGCTGTCTGTCTATCTGTGGATCTCTGCAATAGTCTTGGAGGACCAAAA 975

QY      601  GTCAGGGAAGAGCTCGATGTATTGAGTGTCTTTCAGTGTCCCTTGCAAGTCCAGATGATCTCC 660
DB      976  GTCAGGGAAGAGCTCGATGTATTGAGTGTCTTTCAGTGTCCCTTGCAAGTCCAGATGATCTCC 1035

QY      661  TGGTGGGACCTTTTATGAAGATCTGGCTTTTCACTTTTGGCTTTCGATGATCCCTGTCTC 720
DB      1036  TGGTGGGACCTTTTATGAAGATCTGGCTTTTCACTTTTGGCTTTCGATGATCCCTGTCTC 1095

QY      721  ATCATCATCGTCTGTACACCTGATGATCTGCGCTCTCAAGAGGCTCCGGCTCTCTTCT 780
DB      1096  ATCATCATCGTCTGTACACCTGATGATCTGCGCTCTCAAGAGGCTCCGGCTCTCTTCT 1155

; Publication No. US200400904584
; Sequence 3, Application US/09904584
; Publication No. US200400907704A1
; GENERAL INFORMATION:
; APPLICANT: Kreek, Mary Jeanne
; APPLICANT: Yuforov, Vadim
; APPLICANT: LaForge, Karl Steven
; TITLE OF INVENTION: Alleles of the Human Kappa Opioid
; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods Using Said Alleles, and
; TITLE OF INVENTION: Methods of Treatment Based Thereon
; FILE REFERENCE: 600-1-285N
; CURRENT APPLICATION NUMBER: US/09/904,584
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/218,300
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: homo sapiens
; US-09-904-584-3

Query Match      99.7%; Score 1150.8; DB 11; Length 1154;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  ATGGACTCCCGATCCAGATCTTCCGGGGAGCGCGCCCTACCTGCGCCCGCGAGCGCC 60
DB      1  ATGGACTCCCGATCCAGATCTTCCGGGGAGCGCGCCCTACCTGCGCCCGCGAGCGCC 60

QY      61  TGGCTGCCCCCAACAGCAGCGCTGGTTTCCGGCTGGGCGGAGCCCGACAGCAACGGC 120
DB      61  TGGCTGCCCCCAACAGCAGCGCTGGTTTCCGGCTGGGCGGAGCCCGACAGCAACGGC 120

QY      121  AGCCCGGCTCGGAGGAGCGCGAGCTGGAGCCCGCGCACATCTCCCGCGCATCCCGGTC 180
DB      121  AGCCCGGCTCGGAGGAGCGCGAGCTGGAGCCCGCGCACATCTCCCGCGCATCCCGGTC 180

QY      181  ATCATCATCGGCGTCTACTCCGTAGTGTTCGTGGTGGTGGTGGGCAACTCGCTGGTC 240
DB      181  ATCATCATCGGCGTCTACTCCGTAGTGTTCGTGGTGGTGGTGGGCAACTCGCTGGTC 240
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Qy 241 ATGTTCTGTCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAAC 300
Db 241 ATGTTCTGTCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAAC 300
Qy 301 CTGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
Db 301 CTGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCCCTTTCAGAGTACGGTCTACTTG 360
Qy 361 ATGAATCTCTGGCCCTTTTGGGGATGTGCTGTGCAAGATAGTAAATTTCCATTTGATTACTAC 420
Db 361 ATGAATCTCTGGCCCTTTTGGGGATGTGCTGTGCAAGATAGTAAATTTCCATTTGATTACTAC 420
Qy 421 AACATGTTACACAGATCTTACCTTGACCATGATGAGCGTGGACCGCTACATTTGCCGTG 480
Db 421 AACATGTTACACAGATCTTACCTTGACCATGATGAGCGTGGACCGCTACATTTGCCGTG 480
Qy 481 TGCCACCCCGTGAAGGCTTTGACCTTCGCGACACCCCTTGAAGGCAAGATCATCAATATC 540
Db 481 TGCCACCCCGTGAAGGCTTTGACCTTCGCGACACCCCTTGAAGGCAAGATCATCAATATC 540
Qy 541 TGCATCTGGCTGTCTGTCTCATCTGTGTCATCTCTGCAATAGTCTTGGAGGCAACAAA 600
Db 541 TGCATCTGGCTGTCTGTCTCATCTGTGTCATCTCTGCAATAGTCTTGGAGGCAACAAA 600
Qy 601 GTACGGGAAGACGTGATGTCATTTAGTGCTCTCTGAGTCTTCCAGATGATGATCTCC 660
Db 601 GTACGGGAAGACGTGATGTCATTTAGTGCTCTCTGAGTCTTCCAGATGATGATCTCC 660
Qy 661 TGTGGGACCTCTTCATGAAGATCTGGCTGTTCATCTTTGCTTCTGTCATCTCTGCTC 720
Db 661 TGTGGGACCTCTTCATGAAGATCTGGCTGTTCATCTTTGCTTCTGTCATCTCTGCTC 720
Qy 721 ATCATATCTGTCTGTCTACACCTGATGATCTGCTGCTCTCAAGAGCGTCCGCTCTTCT 780
Db 721 ATCATATCTGTCTGTCTACACCTGATGATCTGCTGCTCTCAAGAGCGTCCGCTCTTCT 780
Qy 781 GGCTCCGAGAGAAGATCGCAACCTGGTGTAGGATCACAGACTGGTCTGGTGGTGGT 840
Db 781 GGCTCCGAGAGAAGATCGCAACCTGGTGTAGGATCACAGACTGGTCTGGTGGTGGT 840
Qy 841 GCAGTCTCTGTCTGTCTGACCTCCCATTCACATATTCATCTCTGCTGGAGGCTCTGGG 900
Db 841 GCAGTCTCTGTCTGTCTGACCTCCCATTCACATATTCATCTCTGCTGGAGGCTCTGGG 900
Qy 901 AGCACTCTCCACAGCAGCTGTCTCTCAGCTATTAATCTCTGATGCTCTTAGGCTAT 960
Db 901 AGCACTCTCCACAGCAGCTGTCTCTCAGCTATTAATCTCTGATGCTCTTAGGCTAT 960
Qy 961 ACCAACAGTAGCTGAATCCCATTTCTAGCGCTTTCTTGATGAAACTTCAAGCGGTG 1020
Db 961 ACCAACAGTAGCTGAATCCCATTTCTAGCGCTTTCTTGATGAAACTTCAAGCGGTG 1020
Qy 1021 TTCCGGGACTTCTGCTTCCACTGAAGATGAGGATGAGCGGCGAGCAGCTAGCAGATC 1080
Db 1021 TTCCGGGACTTCTGCTTCCACTGAAGATGAGGATGAGCGGCGAGCAGCTAGCAGATC 1080
Qy 1081 CGAAATACAGTTACAGGATCTGCTTACCTGAGGACATCGATGGATGAATAAACACAGTA 1140
Db 1081 CGAAATACAGTTACAGGATCTGCTTACCTGAGGACATCGATGGATGAATAAACACAGTA 1140
Qy 1141 TGACTAGTCGTGGA 1154
Db 1141 TGACTAGTCGTGGA 1154
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RESULT 6  
US-09-904-584-4  
; Sequence 4, Application US/09904584  
; Publication No. US20040097704A1  
; GENERAL INFORMATION:  
; APPLICANT: Kreek, Mary Jeanne  
; APPLICANT: Yufarov, Vadim  
; APPLICANT: LaForge, Karl Steven

; TITLE OF INVENTION: Alleles of the Human Kappa Opioid  
; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods Using Said Alleles, and  
; TITLE OF INVENTION: Methods of Treatment Based Thereon  
; FILE REFERENCE: 600-1-285N  
; CURRENT APPLICATION NUMBER: US/09/904,584  
; CURRENT FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: 60/218,300  
; PRIOR FILING DATE: 2000-07-14  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 1154  
; TYPE: DNA  
; ORGANISM: homo sapiens  
; US-09-904-584-4

Query Match 99.7%; Score 1150.8; DB 11; Length 1154;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 ATGACTCTCCCGATCCAGATCTTCCGCGGGAGCGGGCCCTACTCTGCGCCCGAGCGCC 60  
Db 1 ATGACTCTCCCGATCCAGATCTTCCGCGGGAGCGGGCCCTACTCTGCGCCCGAGCGCC 60  
Qy 61 TGCTGCCCCCAACACAGCAGCGCTGTTTCCCGGCTGGGCGAGCCGACAGCAACGGC 120  
Db 61 TGCTGCCCCCAACACAGCAGCGCTGTTTCCCGGCTGGGCGAGCCGACAGCAACGGC 120  
Qy 121 AGCGCGGCTCGGAGGAGCGGAGCTGGAGCGCGGCACATCTCCCGGCGCATCCCGGTC 180  
Db 121 AGCGCGGCTCGGAGGAGCGGAGCTGGAGCGCGGCACATCTCCCGGCGCATCCCGGTC 180  
Qy 181 ATCATACGCGGCTCTACTCCGTAGTGTCTCGTGGGCTTGGTGGGCAACTCCGTC 240  
Db 181 ATCATACGCGGCTCTACTCCGTAGTGTCTCGTGGGCTTGGTGGGCAACTCCGTC 240  
Qy 241 ATGTTCTGTATCATCTCCGATACAAAGATGAAGACAGCAACCAACATTTACATATTTAAAC 300  
Db 241 ATGTTCTGTATCATCTCCGATACAAAGATGAAGACAGCAACCAACATTTACATATTTAAAC 300  
Qy 301 CTGGCTTTGCGAGATGCTTTAGTTACTACAAACCATGCCCTTTCAGAGTACGGTCTACTTG 360  
Db 301 CTGGCTTTGCGAGATGCTTTAGTTACTACAAACCATGCCCTTTCAGAGTACGGTCTACTTG 360  
Qy 361 ATGAATCTCTGGCCCTTTTGGGGATGTGCTGTGCAAGATAGTAAATTTCCATTTGATTACTAC 420  
Db 361 ATGAATCTCTGGCCCTTTTGGGGATGTGCTGTGCAAGATAGTAAATTTCCATTTGATTACTAC 420  
Qy 421 AACATGTTACACAGATCTTTCACCTTGACCATGATGAGCGTGGACCGCTACATTTGCCGTG 480  
Db 421 AACATGTTACACAGATCTTTCACCTTGACCATGATGAGCGTGGACCGCTACATTTGCCGTG 480  
Qy 481 TGCCACCCCGTGAAGGCTTTGAGCTTCCGACACCCCTTGAAGGCAAGATCATCAATATC 540  
Db 481 TGCCACCCCGTGAAGGCTTTGAGCTTCCGACACCCCTTGAAGGCAAGATCATCAATATC 540  
Qy 541 TGATCTGGCTGTCTGTCTCATCTGTGTCATCTCTGCAATAGTCTTGGAGGCAACAAA 600  
Db 541 TGATCTGGCTGTCTGTCTCATCTGTGTCATCTCTGCAATAGTCTTGGAGGCAACAAA 600  
Qy 601 GTACGGGAAGACGTGATGTCATTTAGTGCTCTCTGAGTCTTCCAGATGATGATCTCC 660  
Db 601 GTACGGGAAGACGTGATGTCATTTAGTGCTCTCTGAGTCTTCCAGATGATGATCTCC 660  
Qy 661 TGTGGGACCTCTTCATGAAGATCTGGCTGTTCATCTTTGCTTCTGTCATCTCTGCTC 720  
Db 661 TGTGGGACCTCTTCATGAAGATCTGGCTGTTCATCTTTGCTTCTGTCATCTCTGCTC 720  
Qy 721 ATCATATCTGTCTGTCTACACCTGATGATCTGCTGCTCTCAAGAGCGTCCGCTCTTCT 780  
Db 721 ATCATATCTGTCTGTCTACACCTGATGATCTGCTGCTCTCAAGAGCGTCCGCTCTTCT 780  
Qy 781 GGCTCCGAGAGAAGATCGCAACCTGGTGTAGGATCACAGACTGGTCTGGTGGTGGT 840

Db	781	GGCTCCGAGAGAAAGATCGCAACTCGTAGGATCACAGACTGGTCTCTGGTGGTGGTG	840
Qy	841	GCAGTCTTCGTTGTCTGCTGAGTCCCAATTCACATATTCACTCTGGTGGAGGCTCTGGG	900
Db	841	GCAGTCTTCGTCGTCTGCTGAGTCCCAATTCACATATTCACTCTGGTGGAGGCTCTGGG	900
Qy	901	AGCACCTCCACACAGCAGCAGTGTCTCTCAGACTATTACTTCTGCATCGCCTTAGGCTAT	960
Db	901	AGCACCTCCACACAGCAGTGTCTCTCAGACTATTACTTCTGCATCGCCTTAGGCTAT	960
Qy	961	ACCAACAGTAGCCTGAATCCATTCTCTAGCCCTTTCTTGATGAAAACCTTCAAGCGGTGT	1020
Db	961	ACCAACAGTAGCCTGAATCCATTCTCTAGCCCTTTCTTGATGAAAATTTCAAGCGGTGT	1020
Qy	1021	TTCCGGGACTTCTGCTTTTCCACTGAAGATGAGGATGGAGCGGCAGAGCACTAGCAGAGTC	1080
Db	1021	TTCCGGGACTTCTGCTTTTCCACTGAAGATGAGGATGGAGCGGCAGAGCACTAGCAGAGTC	1080
Qy	1081	CGAATAACAGTTACAGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAAGTA	1140
Db	1081	CGAATAACAGTTACAGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAAGTA	1140
Qy	1141	TGACTAGTCGTGGA	1154
Db	1141	TGACTAGTCGTGGA	1154

## RESULT 7

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US-09-904-584-5
; Sequence 5, Application US/09904584
; Publication No. US20040097704A1
; GENERAL INFORMATION:
; APPLICANT: Kreek, Mary Jeanne
; APPLICANT: Yuferov, Vadim
; APPLICANT: LaForge, Karl Steven
; TITLE OF INVENTION: Alleles of the Human Kappa Opioid
; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods
; TITLE OF INVENTION: Methods of Treatment Based Thereon
; FILE REFERENCE: 600-1-285N
; CURRENT APPLICATION NUMBER: US/09/904,584
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/218,300
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-904-584-5

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RESULT 8
US-9-304-584-6
; Sequence 6, Application US/09904584
; Publication No. US20040097704A1
; GENERAL INFORMATION:
; APPLICANT: Kreek, Mary Jeanne
; APPLICANT: Yufarov, Vadim
; APPLICANT: LaForge, Karl Steven
; TITLE OF INVENTION: Alleles of the

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241	Db	ATGTTCTGGTGATCATCCGATACAAAGATGAAGACAGCAACCAATTTACAATTTAAAC	300
301	Qy	CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCCTTTCAGAGTACGGTCTACTTGG	360
301	Db	CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCAGAGTACGGTCTACTTGG	360
361	Qy	ATGAATTCCTGCGCTTTTGGGGATGTGCTGCAAGATAGTAAATTTCCAATGATTACTATC	420
361	Db	ATGAATTCCTGCGCTTTTGGGGATGTGCTGCAAGATAGTAAATTTCCAATGATTACTATC	420
421	Qy	ACATGTTTCACACAGCATCTTCACCTTTGACCATGATGAGCGTGGACCGCTTACATGTCGGTG	480
421	Db	ACATGTTTCACACAGCATCTTCACCTTTGACCATGATGAGCGTGGACCGCTTACATGTCGGTG	480
481	Qy	TGCCACCCCGTGAAGGCTTTGGACTTCGCGACACCCCTTGAAGGCAAAAGATCATCAATATC	540
481	Db	TGCCACCCCGTGAAGGCTTTGGACTTCGCGACACCCCTTGAAGGCAAAAGATCATCAATATC	540
541	Qy	TGGATCTGGCTGCTGCTGCTCATCTGTTGGCATCTTCGCAATAGTCTTGGAGGCAACCAAA	600
541	Db	TGCATCTGGCTGCTGCTGCTCATCTGTTGGCATCTTCGCAATAGTCTTGGAGGCAACCAAA	600
601	Qy	GTCAAGGAAGACGTGATGTCTATTCAGATGCTCTCTTGCAGTTCGCCAGATGATGACTCTCC	660
601	Db	GTCAAGGAAGACGTGATGTCTATTCAGATGCTCTCTTGCAGTTCGCCAGATGATGACTCTCC	660
661	Qy	TGGTGGGACCTCTTCATGAAGATCTGGGCTTCTCATCTTTGGCCTTTCGTGATCCCTGTCTC	720
661	Db	TGGTGGGACCTCTTCATGAAGATCTGGGCTTCTCATCTTTGGCCTTTCGTGATCCCTGTCTC	720
721	Qy	ATCATCATCGTCTGCTACACCCCTGATGATCTCGGCTCTCAAGAGCGTCCGGCTCTTTCT	780
721	Db	ATCATCATCGTCTGCTACACCCCTGATGATCTCGGCTCTCAAGAGCGTCCGGCTCTTTCT	780
781	Qy	GGCTCCCGAGAGAAAGATCGCAACCTCGTAGGATCAACAGACTGGTCTCTGTGTGTGGTG	840
781	Db	GGCTCCCGAGAGAAAGATCGCAACCTCGTAGGATCAACAGACTGGTCTCTGTGTGTGGTG	840
841	Qy	GCAGTCTTGGTTGTCTGCTGGACTCCCATTCATATTCATCTGTGTGAGGCTCTGCGG	900
841	Db	GCAGTCTTGGTTGTCTGCTGGACTCCCATTCATATTCATCTGTGTGAGGCTCTGCGG	900
901	Qy	AGCACTTCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCACTCGCTTTAGGCTAT	960
901	Db	AGCACTTCCACAGCACAGCTGCTCTCTCCAGCTATTACTTCTGCACTCGCTTTAGGCTAT	960
961	Qy	ACCAACAGTAGCTGAATCCCATCTCTAGCCCTTTCTTGAAGAAAACCTTCAAGCGGTGT	1020
961	Db	ACCAACAGTAGCTGAATCCCATCTCTAGCCCTTTCTTGAAGAAAACCTTCAAGCGGTGT	1020
1021	Qy	TTCCGGGACTTCGCTTTCCACTGAAGATGAGGATGGAGCGGCAGAGCACTAGCAGATC	1080
1021	Db	TTCCGGGACTTCGCTTTCCACTGAAGATGAGGATGGAGCGGCAGAGCACTAGCAGATC	1080
1081	Qy	CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACAGTA	1140
1081	Db	CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACAGTA	1140
1141	Qy	TGACTAGTCTGGGA	1154
1141	Db	TGACTAGTCTGGGA	1154

2



;; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods Using Said Alleles, and  
;; FILE REFERENCE: 600-1-285N  
;; CURRENT APPLICATION NUMBER: US/09/904,584  
;; CURRENT FILING DATE: 2001-07-13  
;; PRIOR APPLICATION NUMBER: 60/218,300  
;; PRIOR FILING DATE: 2000-07-14  
;; NUMBER OF SEQ ID NOS: 7  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 6  
;; LENGTH: 1154  
;; TYPE: DNA  
;; ORGANISM: homo sapiens  
US-09-904-584-6

Query Match 99.7%; Score 1150.8; DB 11; Length 1154;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGACTCCCGATCCAGATCTTCGGGGGAGCGGGCCCTACTCGGCCCGGAGCGCC 60  
Db 1 ATGACTCCCGATCCAGATCTTCGGGGGAGCGGGCCCTACTCGGCCCGGAGCGCC 60

Qy 61 TGCCTGCCCCCAACAGCAGCGCTGTTTCCCGCTGGGCGGAGCGCCAGCAACGGC 120  
Db 61 TGCCTGCCCCCAACAGCAGCGCTGTTTCCCGCTGGGCGGAGCGCCAGCAACGGC 120

Qy 121 AGCCCGGCTCGGAGGAGCGCAGCTGGAGCGCGCACATCTCCCGGCCATCCCGGTC 180  
Db 121 AGCCCGGCTCGGAGGAGCGCAGCTGGAGCGCGCACATCTCCCGGCCATCCCGGTC 180

Qy 181 ATCATCAGCGGGCTACTCCGTAGTGTTCGTGCGGGCTTGGTGGGCACTCGCTGGTC 240  
Db 181 ATCATCAGCGGGCTACTCCGTAGTGTTCGTGCGGGCTTGGTGGGCACTCGCTGGTC 240

Qy 241 ATGTTCTGTATCCCGATACAAAGATGAAGACAGCAACCAATTTACATATTAAAC 300  
Db 241 ATGTTCTGTATCCCGATACAAAGATGAAGACAGCAACCAATTTACATATTAAAC 300

Qy 301 CTGCTTTGGCAGATGCTTTAGTTAGTACTACACCATGCGCTTTCAGATGAGGTCTACTG 360  
Db 301 CTGCTTTGGCAGATGCTTTAGTTAGTACTACACCATGCGCTTTCAGATGAGGTCTACTG 360

Qy 361 ATGAATTCCTGGCCCTTTGGGATGTCTGTGCAAGATAGTAATTTCCATTTACTATC 420  
Db 361 ATGAATTCCTGGCCCTTTGGGATGTCTGTGCAAGATAGTAATTTCCATTTACTATC 420

Qy 421 AACATGTTCCACGATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTTGCCGTG 480  
Db 421 AACATGTTCCACGATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTTGCCGTG 480

Qy 481 TGCCACCCCGTGAAGGCTTTGGATCTCGCACACCTTTGAGGCAAGATCATCAATATC 540  
Db 481 TGCCACCCCGTGAAGGCTTTGGATCTCGCACACCTTTGAGGCAAGATCATCAATATC 540

Qy 541 TGCAATCTGGCTGCTGCTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGACCAAA 600  
Db 541 TGCAATCTGGCTGCTGCTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGACCAAA 600

Qy 601 GTCAGGAAGACGTCGATGTCATTTAGTGTCTTTCAGATTTCCAGATGATGACTATCC 660  
Db 601 GTCAGGAAGACGTCGATGTCATTTAGTGTCTTTCAGATTTCCAGATGATGACTATCC 660

Qy 661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTTCATCTTTGCTTTCGTGATCCCTGCTC 720  
Db 661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTTCATCTTTGCTTTCGTGATCCCTGCTC 720

Qy 721 ATCATATCTGCTCTACACCTGATGATCTGCTGCTCTCAAGAGCGTCCGCTCTTCT 780  
Db 721 ATCATATCTGCTCTACACCTGATGATCTGCTGCTCTCAAGAGCGTCCGCTCTTCT 780

Qy 781 GGCTCCCGAGAAAGATCGCAACCTCGTAGGATCACAGACTGGTCTCGTGGTGGTG 840  
Db 781 GGCTCCCGAGAAAGATCGCAACCTCGTAGGATCACAGACTGGTCTCGTGGTGGTG 840

Db 781 GGCTCCCGAGAAAGATCGCAACCTCGTAGGATCACAGACTGGTCTCGTGGTGGTG 840  
Qy 841 GCACTCTTCGTTGCTCTGGACTCCCAATTCACATATTCATCTCTGGTGGAGGCTCTGGGG 900  
Db 841 GCGGTCTTCGTTGCTCTGGACTCCCAATTCACATATTCATCTCTGGTGGAGGCTCTGGGG 900

Qy 901 AGCACTCCACAGCAGCTGCTCTCCAGCTATTACTTCTGCATCGCTTATAGGCTAT 960  
Db 901 AGCACTCCACAGCAGCTGCTCTCCAGCTATTACTTCTGCATCGCTTATAGGCTAT 960

Qy 961 ACCAACAAGTAGCCTGAATCCATTTCTACGCCCTTTCTTGATGAAAATCTCAAGCGGTG 1020  
Db 961 ACCAACAAGTAGCCTGAATCCATTTCTACGCCCTTTCTTGATGAAAATCTCAAGCGGTG 1020

Qy 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGCGGACAGCACTAGCAGAGTC 1080  
Db 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGCGGACAGCACTAGCAGAGTC 1080

Qy 1081 CGAAATACAGTTCCAGGATCTGCTTACTCTGAGGACATCGATGGATGAATAAACAGTA 1140  
Db 1081 CGAAATACAGTTCCAGGATCTGCTTACTCTGAGGACATCGATGGATGAATAAACAGTA 1140

Qy 1141 TGACTAGTCTGGA 1154  
Db 1141 TGACTAGTCTGGA 1154

RESULT 9  
US-09-904-584-7  
; Sequence 7, Application US/09904584  
; Publication No. US20040097704A1  
; GENERAL INFORMATION:  
; APPLICANT: Kreek, Mary Jeanne  
; APPLICANT: Yufetov, Vadim  
; APPLICANT: LaForge, Karl Steven  
; TITLE OF INVENTION: Alleles of the Human Kappa Opioid  
; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods Using Said Alleles, and  
; TITLE OF INVENTION: Methods of Treatment Based Thereon  
; FILE REFERENCE: 600-1-285N  
; CURRENT APPLICATION NUMBER: US/09/904,584  
; CURRENT FILING DATE: 2001-07-13  
; PRIOR FILING DATE: 60/218,300  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 1154  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-09-904-584-7

Query Match 99.7%; Score 1150.8; DB 11; Length 1154;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGACTCCCGATCCAGATCTTCGGGGGAGCGGGCCCTACTCGGCCCGGAGCGCC 60  
Db 1 ATGACTCCCGATCCAGATCTTCGGGGGAGCGGGCCCTACTCGGCCCGGAGCGCC 60

Qy 61 TGCCTGCCCCCAACAGCAGCGCTGTTTCCCGCTGGGCGGAGCGCCAGCAACGGC 120  
Db 61 TGCCTGCCCCCAACAGCAGCGCTGTTTCCCGCTGGGCGGAGCGCCAGCAACGGC 120

Qy 121 AGCCCGGCTCGGAGGAGCGCAGCTGGAGCGCGCACATCTCCCGGCCATCCCGGTC 180  
Db 121 AGCCCGGCTCGGAGGAGCGCAGCTGGAGCGCGCACATCTCCCGGCCATCCCGGTC 180

Qy 181 ATCATCAGCGGGCTACTCCGTAGTGTTCGTGCGGGCTTGGTGGGCACTCGCTGGTC 240  
Db 181 ATCATCAGCGGGCTACTCCGTAGTGTTCGTGCGGGCTTGGTGGGCACTCGCTGGTC 240

Qy 241 ATGTTCTGTATCCCGATACAAAGATGAAGACAGCAACCAATTTACATATTAAAC 300  
Db 241 ATGTTCTGTATCCCGATACAAAGATGAAGACAGCAACCAATTTACATATTAAAC 300



241 ATGTTCTGATCATCCGATACACAAAGATGAAGACACCAACCAATTTACATATTTAAAC 300  
301 CTGGCTTTGGCAGATGCTTTAGTACTACCAACATGCGCTTTTCAGAGTAGGCTCTACTTG 360  
301 CTGGCTTTGGCAGATGCTTTAGTACTACCAACATGCGCTTTTCAGAGTAGGCTCTACTTG 360  
361 ATGAATTCCTGGCTTTGGGATGCTGTGCAAGATAGTAAATTTCCATTTGATTAATAC 420  
361 ATGAATTCCTGGCTTTGGGATGCTGTGCAAGATAGTAAATTTCCATTTGATTAATAC 420  
421 AACATGTTCCACAGCATCTTCACTTTGACCATGATGAGCGTGACCGCTACATTAATTC 480  
421 AACATGTTCCACAGCATCTTCACTTTGACCATGATGAGCGTGACCGCTACATTAATTC 480  
481 TGGCACCCTGGTGAAGCTTTGGACCTTCCGACACCCCTTGAAGCAAAAGATCATCAATATC 540  
481 TGGCACCCTGGTGAAGCTTTGGACCTTCCGACACCCCTTGAAGCAAAAGATCATCAATATC 540  
541 TGATCTGGCTGTGCTGCTCATCTGTTGGCATCTCTGCAATAGTCTCTGGAGGACCAAAA 600  
541 TGATCTGGCTGTGCTGCTCATCTGTTGGCATCTCTGCAATAGTCTCTGGAGGACCAAAA 600  
601 GTGAGGAAAGACGTGATGCTCAATGAGTGTCTCTGAGTTCCTGAGTCCAGATGATGACTCC 660  
601 GTGAGGAAAGACGTGATGCTCAATGAGTGTCTCTGAGTTCCTGAGTCCAGATGATGACTCC 660  
661 TGGTGGGACCTCTTCAATGAAGATCTGCTGCTTTCATCTTTGCTTTCATCTGATCCCTGCTC 720  
661 TGGTGGGACCTCTTCAATGAAGATCTGCTGCTTTCATCTTTGCTTTCATCTGATCCCTGCTC 720  
721 ATCATCATGCTGCTGCTACACCTTGATGCTCTGCTGCTCAAGAGCTCTCGGCTCTCTTCT 780  
721 ATCATCATGCTGCTGCTACACCTTGATGCTCTGCTGCTCAAGAGCTCTCGGCTCTCTTCT 780  
781 GGCTCCGAGAGAAAGATCGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
781 GGCTCCGAGAGAAAGATCGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
841 GCAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
841 GCAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
901 AGCAGCTCCACAGCAGCTGCTCTCTCCAGTATTAATTTCTGCTGCTGCTGCTGCTGCTAT 960  
901 AGCAGCTCCACAGCAGCTGCTCTCTCCAGTATTAATTTCTGCTGCTGCTGCTGCTAT 960  
961 ACCAAGTAGCTGAATCCCATCTCTAGCGCTTTCTGATGAAATTTCAAGCGGTGT 1020  
961 ACCAAGTAGCTGAATCCCATCTCTAGCGCTTTCTGATGAAATTTCAAGCGGTGT 1020  
1021 TTCCGGGACTTCTGCTTCTCCACTGAAGATGAGGATGAGGCGGAGAGCTAGCAGATC 1080  
1021 TTCCGGGACTTCTGCTTCTCCACTGAAGATGAGGATGAGGCGGAGAGCTAGCAGATC 1080  
1081 CGAATAACAGTTCAGGATCTGCTTACCTGAGGACATCGATGGGATGAATAACCAAGTA 1140  
1081 CGAATAACAGTTCAGGATCTGCTTACCTGAGGACATCGATGGGATGAATAACCAAGTA 1140  
1141 TGACTAGTCTGTGA 1154  
1141 TGACTAGTCTGTGA 1154

RESULT 10  
US-10-225-567A-147  
; Sequence 147, Application US/10225567A  
; Publication No. US20030113798A1  
; GENERAL INFORMATION:  
; APPLICANT: LifeSpan Biosciences  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burner, Glenna C.  
; APPLICANT: Roush, Christine L.  
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS

FILE REFERENCE: 1920-4-4  
; CURRENT APPLICATION NUMBER: US/10/225,567A  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/257,144  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 2292  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 147  
; LENGTH: 1182  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-225-567A-147

Query Match 99.2%; Score 1144.4; DB 15; Length 1182;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 1148; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGGACTCCCGATCCAGATCTTCCGCGGGAGCGGCGCTTACCTGCGCCCGAGCGCC 60  
DB 14 ATGGATCCCGATCCAGATCTTCCGCGGGAGCGCTTACCTGCGCCCGAGCGCC 73  
QY 61 TGCCTGCCCGCCCAACAGCAGCGCTGCTGCTTCCGCGCTGGGCGAGCCCGACAGCAACGGC 120  
DB 74 TGCCTGCCCGCCCAACAGCAGCGCTGCTGCTTCCGCGCTGGGCGAGCCCGACAGCAACGGC 133  
QY 121 AGCGCGGCTCGAGAGCGCGCAGCTGGAGCGCGGCACATCTCCCGGCGCATCCCGGTC 180  
DB 134 AGCGCGGCTCGAGAGCGCGCAGCTGGAGCGCGGCACATCTCCCGGCGCATCCCGGTC 193  
QY 181 ATCATCACGCGGCTTACTCCGCTAGTGTTCGTGCTGGGCTTGGTGGGCAACTCGCTGTC 240  
DB 194 ATCATCACGCGGCTTACTCCGCTAGTGTTCGTGCTGGGCTTGGTGGGCAACTCGCTGTC 253  
QY 241 ATGTTCTGATCATCCGATACCAAGATGAAGACAGCAACCAATTTACATATTTAAC 300  
DB 254 ATGTTCTGATCATCCGATACCAAGATGAAGACAGCAACCAATTTACATATTTAAC 313  
QY 301 CTGGCTTTGGCAGATGCTTTAGTACTACCAACATGCGCTTTTCAGAGTAGGCTCTACTTG 360  
DB 314 CTGGCTTTGGCAGATGCTTTAGTACTACCAACATGCGCTTTTCAGAGTAGGCTCTACTTG 373  
QY 361 ATGAATTCCTGGCTTTGGGATGCTGTGCAAGATAGTAAATTTCCATTTGATTAATAC 420  
DB 374 ATGAATTCCTGGCTTTGGGATGCTGTGCAAGATAGTAAATTTCCATTTGATTAATAC 433  
QY 421 AACATGTTCCACAGCATCTTCACTTTGACCATGATGAGCGTGACCGCTACATTTGCGGTG 480  
DB 434 AACATGTTCCACAGCATCTTCACTTTGACCATGATGAGCGTGACCGCTACATTTGCGGTG 493  
QY 481 TGGCACCCTGGTGAAGCTTTGGACCTTCCGACACCCCTTGAAGCAAAAGATCATCAATATC 540  
DB 494 TGGCACCCTGGTGAAGCTTTGGACCTTCCGACACCCCTTGAAGCAAAAGATCATCAATATC 553  
QY 541 TGATCTGGCTGTGCTGCTCATCTGTTGGCATCTCTGCAATAGTCTCTGGAGGACCAAAA 600  
DB 554 TGATCTGGCTGTGCTGCTCATCTGTTGGCATCTCTGCAATAGTCTCTGGAGGACCAAAA 613  
QY 601 GTGAGGAAAGACGTGATGCTCAATGAGTGTCTCTGAGTTCCTGAGTCCAGATGATGACTACTC 660  
DB 614 GTGAGGAAAGACGTGATGCTCAATGAGTGTCTCTGAGTTCCTGAGTCCAGATGATGACTACTC 673  
QY 661 TGGTGGGACCTCTTCAATGAAGATCTGCTGCTTTCATCTTTGCTTTCATCTTGGCTTCCCTGCTC 720  
DB 674 TGGTGGGACCTCTTCAATGAAGATCTGCTGCTTTCATCTTTGCTTTCATCTTGGCTTCCCTGCTC 733  
QY 721 ATCATCATGCTCTGCTACACCTTGATGCTCTGCTGCTCAAGAGCTCTCGGCTCTCTTCT 780  
DB 734 ATCATCATGCTCTGCTACACCTTGATGCTCTGCTGCTCAAGAGCTCTCGGCTCTCTTCT 793  
QY 781 GGCTCCGAGAGAAAGATCGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840  
DB 794 GGCTCCGAGAGAAAGATCGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 853

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Qy 941 GCACTCTTGTGTCTGTCTGACTCCCATTCACATATTCATCTCTGGTGGAGGCTCTGGGG 900
Db 854 GCGGTTTTCTGTCGTCTGTGACTCCCATTCACATATTCATCTCTGGTGGAGGCTCTGGGG 913
Qy 901 AGCACTCTCCACACAGAGCTGTCTCTCCAGCTATTACTTCTGCATCGCTTAGGCTAT 960
Db 914 AGCACTCTCCACACAGAGCTGTCTCTCCAGCTATTACTTCTGCATCGCTTAGGCTAT 973
Qy 961 ACCAACAGTAGCTGAATCCCATTTCTCTACGCCCTTTCTTGATGAAAACTTCAAGCGGTGT 1020
Db 974 ACCAACAGTAGCTGAATCCCATTTCTCTACGCCCTTTCTTGATGAAAACTTCAAGCGGTGT 1033
Qy 1021 TTCCGGGACTTCTGCTTTTCCACTGAAGATGAGGATGAGCGGACAGCACTAGCAGATC 1080
Db 1034 TTCCGGGACTTCTGCTTTTCCACTGAAGATGAGGATGAGCGGACAGCACTAGCAGATC 1093
Qy 1081 CGAATACAGTTACAGATCTGCTTACTCTGAGGACATCGATGGATGAATAAACAGTA 1140
Db 1094 CGAATACAGTTACAGATCTGCTTACTCTGAGGACATCGATGGATGAATAAACAGTA 1153
Qy 1141 TGACTAGTCTGTGA 1154
Db 1154 TGACTAGTCTGTGA 1167

RESULT 11
US-10-345-680-19
; Sequence 19, Application US/10345680
; Publication No. US20030148394A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Venkateswarlu, Karicheti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46556, 62553, 302, 323,
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: MPI02-012P1RNM OMNI
; CURRENT APPLICATION NUMBER: US/10/345,680
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/349,511
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414,262
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419,986
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 1182
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (14)...(1156)
US-10-345-680-19
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Query Match 99.2%; Score 1144.4; DB 15; Length 1182;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 1148; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Db 14 ATGGAATCCCGATCCAGATCTTCCGCGGAGAGCTTGGCCCTACCTCGGCCCGGAGCGCC 73
Qy 61 TGCTGCCCCCACAACAGACAGCGCTTGGTTTCCGGCTTGGGCGGAGCGCGACAGCAACGGC 120
Db 74 TGCTGCCCCCACAACAGACAGCGCTTGGTTTCCGGCTTGGGCGGAGCGCGACAGCAACGGC 133
Qy 121 AGGCGCGGCTCGGAGGACGCGAGCTGGAGCCCGGCACATCTCCCGGCCCATCCCGGTC 180
Db 134 AGGCGCGGCTCGGAGGACGCGAGCTGGAGCCCGGCACATCTCCCGGCCCATCCCGGTC 193
Qy 181 ATCATCACGCGGCTCTACTCCGTAAGTTCGTGCTGGGCTTGGTGGCAACTCCGCTGTC 240
Db 194 ATCATCACGCGGCTCTACTCCGTAAGTTCGTGCTGGGCTTGGTGGCAACTCCGCTGTC 253
Qy 241 ATGTTGCTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
Db 254 ATGTTGCTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 313
Qy 301 TGCTGTTGGCAGATGCTTTAGTTACTACCAACATGCCCCTTTCAGAGTACGGTCTACTTG 360
Db 314 CTGGCTTTGGCAGATGCTTTAGTTACTACCAACATGCCCCTTTCAGAGTACGGTCTACTTG 373
Qy 361 ATGAATTCCTGGCCTTTTGGGATGTGCTGTGCAAGATAGTAATTTCCATTTGATTTAC 420
Db 374 ATGAATTCCTGGCCTTTTGGGATGTGCTGTGCAAGATAGTAATTTCCATTTGATTTAC 433
Qy 421 AACATGTTTACCAGATCTTTCACTTGACCATGATGAGCGTGGACCGCTACATTTGCCGTG 480
Db 434 AACATGTTTACCAGATCTTTCACTTGACCATGATGAGCGTGGACCGCTACATTTGCCGTG 493
Qy 481 TGCACCCCGTGAAGGCTTTGGGACTCCCGCACACCCCTTGAAGGCAAAAGATCATCAATATC 540
Db 494 TGCACCCCGTGAAGGCTTTGGGACTCCCGCACACCCCTTGAAGGCAAAAGATCATCAATATC 553
Qy 541 TGCACTGCGTGTCTGCTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGACCAAA 600
Db 554 TGCACTGCGTGTCTGCTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGACCAAA 613
Qy 601 GTGAGGGAAGACGTGATGTCTGATGCTCTCTTGAGTTCAGATGATGATGATGATGATGAT 660
Db 614 GTGAGGGAAGACGTGATGTCTGATGCTCTCTTGAGTTCAGATGATGATGATGATGATGAT 673
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Db 674 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCTTTCGATGATGATGATGATGAT 733
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Db 734 ATCATCATCTGCTCTACACCCCTGATGATCTGCGTCTCAAGAGCGTCCGCTCTCTTCT 793
Qy 781 GGCTCCCGAGAGAAAGATCCGAACCTCGGTAGGATACACAGATGCTGCTGCTGGTGGTGGTG 840
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Db 854 GCGGTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 913
Qy 901 AGCACCTCCACACAGCAGCTGCTCTCTCCAGCTATTACTTCTGATCGCTCTAGGCTAT 960
Db 914 AGCACCTCCACACAGCAGCTGCTCTCTCCAGCTATTACTTCTGATCGCTCTAGGCTAT 973
Qy 961 ACCAACAGTAGCTGAATCCCATTTCTAGCGCTTTCTTGATGAAAACTTCAAGCGGTGT 1020
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Db 1034 TTCCGGGACTTCTGCTTTTCCACTGAGATGAGGATGAGCGGACAGCACTAGCAGATC 1093
Qy 1081 CGAAATACAGTTACAGATCTGCTTACTCTGAGGACATCGATGGGATGAATAAACAGTA 1140
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Db 1094 CGAATACAGTTCAGGATCTGCTTACCTGAGGACATCGATGGGATGATATAACAGTA 1153  
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 Db 1154 TGACTAGTCGTGGA 1167

RESULT 12  
 US-10-305-720-1417  
 ; Sequence 1417, Application US/10305720  
 ; Publication No. US20040010136A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.  
 ; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression  
 ; FILE REFERENCE: FA-0002-1 CON  
 ; CURRENT APPLICATION NUMBER: US/10/305,720  
 ; PRIOR FILING DATE: 2002-11-26  
 ; PRIOR APPLICATION NUMBER: 09/016,434  
 ; PRIOR FILING DATE: 1998-01-30  
 ; NUMBER OF SEQ ID NOS: 1490  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 1417  
 ; LENGTH: 1182  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; OTHER INFORMATION: GenBank ID No. US20040010136A1 g532059  
 ; US-10-305-720-1417

Query Match 99.2%; Score 1144.4; DB 17; Length 1182;  
 Best Local Similarity 99.5%; Pred. No. 0;  
 Matches 1148; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGGACTCCCGATCCAGATCTTCCGCGGGAGCCGCGGCCCTACCTGCGCCCGAGCGGC 60  
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 QY 61 TGCTGCCCCCAACAGCAGCGCTGGTTCCCGCTGGGCCGAGCCCGACAGCAAGGC 120  
 Db 74 TGCTGCCCCCAACAGCAGCGCTGGTTCCCGCTGGGCCGAGCCCGACAGCAAGGC 133  
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 Db 134 AGCGCGGCTCGGAGGAGCGGAGCTGGAGCGCGGCACATCTCCCGGCCATCCCGGTC 193  
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 Db 194 ATCATCACGCGGCTTACTCCGTTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC 253  
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 QY 361 ATGAATCTCGGCTTTGGGATGTCGTGCAAGATAGTAAATTTCCATTTGATTTACTAC 420  
 Db 374 ATGAATCTCGGCTTTGGGATGTCGTGCAAGATAGTAAATTTCCATTTGATTTACTAC 433  
 QY 421 AACATGTTCCAGAGATCTTACCTTACCATGATGAGCGTGACCGCTACATTCGCGTG 480  
 Db 434 AACATGTTCCAGAGATCTTACCTTACCATGATGAGCGTGACCGCTACATTCGCGTG 493  
 QY 481 TGCAACCCCGTGAAGGCTTTGGACTTCCGACACCCCTTGAAGGCAAGATCATCAATATC 540  
 Db 494 TGCAACCCCGTGAAGGCTTTGGACTTCCGACACCCCTTGAAGGCAAGATCATCAATATC 553  
 QY 541 TGCAATCTGGCTGTCGTGATCTGTTGGATCTCTGCAATAGTCTTGGAGGACCAAA 600

Db 554 TGCAATCTGGCTGCTGTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGACCAAA 613  
 QY 601 GTCAGGGAAGAGTCGATGTCATTGAGTGTCTCTTGCAGTTTCCAGATGATGATCTCTCC 660  
 Db 614 GTCAGGGAAGAGTCGATGTCATTGAGTGTCTCTTGCAGTTTCCAGATGATGATCTCTCC 673  
 QY 661 TGGTGGGACCTCTTTCATGAAGATCTGCGTCTTTCATCTTTGGCCTTCCGTGTCCTC 720  
 Db 674 TGGTGGGACCTCTTTCATGAAGATCTGCGTCTTTCATCTTTGGCCTTCCGTGTCCTC 733  
 QY 721 ATCATCATGCTCTGTACACCCCTGATGATCTGCGTCTCAAGAGCGTCCGGCTCTCTTCT 780  
 Db 734 ATCATCATGCTCTGTACACCCCTGATGATCTGCGTCTCAAGAGCGTCCGGCTCTCTTCT 793  
 QY 781 GGTCCCGAGAGAAGATGCGAACCTGCTAGGATCACCAGACTGCTCTGTTGGTGGTG 840  
 Db 794 GGTCCCGAGAGAAGATGCGAACCTGCTAGGATCACCAGACTGCTCTGTTGGTGGTG 853  
 QY 841 GCAGTCTTCTGTTGCTGCTGGACTCCCATTCACATATTCATCTCTGTTGGAGGCTCTGGG 900  
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 Db 1154 TGCACTAGTCGTGGA 1167

RESULT 13  
 US-10-283-975A-80  
 ; Sequence 80, Application US/10283975A  
 ; Publication No. US20040110792A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ortho-Clinical Diagnostics, Inc.  
 ; TITLE OF INVENTION: Methods For Assessing and Treating Leukemia  
 ; FILE REFERENCE: CDS 293 PCT  
 ; CURRENT APPLICATION NUMBER: US/10/283,975A  
 ; CURRENT FILING DATE: 2002-10-30  
 ; PRIOR APPLICATION NUMBER: 60/340,938  
 ; PRIOR FILING DATE: 2001-10-30  
 ; PRIOR APPLICATION NUMBER: 60/338,997  
 ; PRIOR FILING DATE: 2001-10-30  
 ; PRIOR APPLICATION NUMBER: 60/340,081  
 ; PRIOR FILING DATE: 2001-10-30  
 ; PRIOR APPLICATION NUMBER: 60/341,012  
 ; PRIOR FILING DATE: 2001-10-30  
 ; NUMBER OF SEQ ID NOS: 900  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 80  
 ; LENGTH: 1182  
 ; TYPE: DNA  
 ; ORGANISM: HUMAN  
 ; US-10-283-975A-80

Query Match 99.2%; Score 1144.4; DB 18; Length 1182;  
 Best Local Similarity 99.5%; Pred. No. 0;  
 Matches 1148; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy 1 ATGGAATCCCGATCCAGATCTTCCGCGGGAGCCGGGCCCTTACCTGGGCCCGGAGCGCC 60
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Db 74 TGCTGCCCCCACCACAGCGCTGCTTCCGGCTGGCGGAGCCCGACAGCAAGCGC 133
Qy 121 AGCGCCGGCTCGGAGGAGCGGAGCTGGAGCCCGCGCACATCTCCCGCGGCATCCCGGTC 180
Db 134 AGCGCCGGCTCGGAGGAGCGGAGCTGGAGCCCGCGCACATCTCCCGCGGCATCCCGGTC 193
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Db 554 TGCATCTGGTGTCTGTCATCTGTTGGATCTCTGCAATAGTCCCTTGGAGGACCAAA 613
Qy 601 GTGAGGAAGACGTCGATGTCATTGAGTGTCTTTCAGTTCCTGAGTTCAGATGATGACTTCC 660
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Db 1094 CGAAATACAGTTACAGGATCCTGCTTACCTGAGGACATCGATGGATGAATAAACCAAGTA 1153
Qy 1141 TGACTAGTCTGTGA 1154
Db 1154 TGACTAGTCTGTGA 1167

RESULT 14
US-10-318-661-1
; Sequence 1, Application US/10318661
; Publication No. US20030167476A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Bruce R.
; TITLE OF INVENTION: Selective Target Cell Activation By
; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated
; TITLE OF INVENTION: Superiorly By Synthetic Ligand
; FILE REFERENCE: UCAL-049CIP2
; CURRENT APPLICATION NUMBER: US/10/318,661
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 09/341,446
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US97/05334
; PRIOR FILING DATE: 1997-03-25
; PRIOR APPLICATION NUMBER: US 08/622,348
; PRIOR FILING DATE: 1996-03-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1143
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-318-661-1

Query Match 98.9%; Score 1141.4; DB 16; Length 1143;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1142; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 61 TGCTGCCCCCACCACAGCGCTGCTTCCGGCTGGCGGAGCCCGACAGCAAGCGC 120
Db 61 TGCTGCCCCCACCACAGCGCTGCTTCCGGCTGGCGGAGCCCGACAGCAAGCGC 120
Qy 121 AGCGCCGGCTCGGAGGAGCGGAGCTGGAGCCCGCGCACATCTCCCGCGGCATCCCGGTC 180
Db 121 AGCGCCGGCTCGGAGGAGCGGAGCTGGAGCCCGCGCACATCTCCCGCGGCATCCCGGTC 180
Qy 181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGTGGGCTTGGTGGCAACTCGCTGGTC 240
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Qy 301 CTGCTTTTGGCAGATGCTTTAGTTACTACAAACCATGCCCCTTTCAGAGTACGGTCTACTTG 360
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Db 481 TGCCACCCCGTGAAGGCTTTGGACTTCGCGACACCCCTTGAAGGCAAAAGATCATCAATATC 540
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 1141 TGA 1143  
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RESULT 15  
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 ; Sequence 3, Application US/10318661  
 ; Publication No. US20030167476A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Conklin, Bruce R.  
 ; TITLE OF INVENTION: Selective Target Cell Activation By  
 ; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated  
 ; FILE OF INVENTION: Superiorly By Synthetic Ligand  
 ; FILE REFERENCE: UCAL-049CIP2  
 ; CURRENT APPLICATION NUMBER: US/10/318,661  
 ; CURRENT FILING DATE: 2003-05-05  
 ; PRIOR APPLICATION NUMBER: US 09/341,446  
 ; PRIOR FILING DATE: 1999-12-20  
 ; PRIOR APPLICATION NUMBER: PCT/US97/05334  
 ; PRIOR FILING DATE: 1997-03-25  
 ; PRIOR APPLICATION NUMBER: US 08/622,348  
 ; PRIOR FILING DATE: 1996-03-26  
 ; NUMBER OF SEQ ID NOS: 28  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 3  
 ; LENGTH: 1284  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: modified KOR  
 US-10-318-661-3

Query Match 98.5%; Score 1136.2; DB 16; Length 1284;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 1138; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
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 QY 62 GCGTCCCGGATCCAGATCTTCCGCGGGAGCCGGGCGCTACCTGCGCGCCGAGCGCA 121  
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 DB 293 TCATCAGCGGCTCTACTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 352  
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 DB 353 TGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTAAAC 412  
 QY 302 TGGCTTTGGGATGCTTTAGTTACTACAAACATGCTGCTGCTGCTGCTGCTGCTGCTGCT 361  
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 DB 533 ACATGTTCCAGAGATCTTACCTTGAAGATGAGGATGAGGATGAGGATGAGGATGAGGAT 592  
 QY 482 GCGACCCGCTGAGGCTTTGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 541  
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Qy	1022	TCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCAGAGCACTAGCAGATCC	1081
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Qy	1082	GAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCACTAT	1141
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Qy	1142	G	1142
Db	1253	G	1253

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Job time : 769.333 secs

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OM nucleic - nucleic search, using sw model

Run on: April 6, 2005, 12:28:42 ; Search time 4384.33 Seconds  
(without alignments)  
10018.893 Million cell updates/sec

Title: US-09-904-584-2  
Perfect score: 1154  
Sequence: 1 atggactcccgatccagat.....ccagatgactagtcgtgga 1154

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST: \*  
1: gb\_est1: \*  
2: gb\_est2: \*  
3: gb\_hc: \*  
4: gb\_est3: \*  
5: gb\_est4: \*  
6: gb\_est5: \*  
7: gb\_est6: \*  
8: gb\_gss1: \*  
9: gb\_gss2: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	803.6	69.6	895	6	CB565888
2	581.8	50.4	762	7	CO960667
3	518.8	45.0	784	7	CO960682
4	470.6	40.8	837	7	CF593603
5	466.4	40.4	480	5	EX092912
6	432.4	37.5	2405	3	AK038389
7	420.3	36.4	4022	3	AK043873
8	367.8	31.9	2919	3	AK038620
9	367.8	31.9	2959	3	AK079529
10	352.0	30.5	879	9	AY410745
11	335.6	29.1	2940	3	AK044178
12	327.4	28.4	2974	3	AK043275
13	327.4	28.3	3101	3	AK031926
14	325.8	28.2	879	9	AY410747
15	309.8	26.8	1053	9	CNS04C2T
16	277.6	24.1	775	5	EX874804
17	274.2	23.8	787	7	CN439929
18	269.8	23.4	888	2	BF676176
19	267.2	23.1	917	5	BU219878
20	264.4	22.9	579	5	BP214141
21	263.8	22.9	579	5	BP213719
22	239.8	20.8	657	2	BB588668
23	231.2	20.0	682	9	AY410746
24	228	19.8	1176	9	AY400827

25	227.4	19.7	389	2	BE649947
26	225	19.5	1176	9	AY400829
27	225	19.5	2014	3	AK046464
28	224.6	19.5	980	4	BM543468
29	223	19.3	632	2	BB641725
30	219.8	19.0	1006	9	AY400676
31	217.6	18.9	784	5	BQ179053
32	215.8	18.7	750	7	CO934661
33	214	18.5	429	4	BM342951
34	213.8	18.5	2432	3	AK051189
35	213.2	18.5	1006	9	AY400674
36	213.2	18.5	2048	3	CR593522
37	213	18.5	836	9	CNS02262
38	211	18.3	866	6	CD246184
39	211	18.3	531	9	CE517843
40	208.6	18.1	877	9	CNS02SC2
41	208.2	18.0	842	9	CNS02SKU
42	207.8	18.0	697	5	BUL39251
43	207.8	18.0	757	5	BU614716
44	206.4	17.9	672	7	CO957761
45	203.4	17.6	785	4	BI754749

ALIGNMENTS

RESULT 1  
LOCUS CB565888 895 bp mRNA linear EST 02-APR-2003  
DEFINITION AGENCOURT12691503 NIH\_MGC146 Homo sapiens cDNA clone  
IMAGE:6519213 5', mRNA sequence.  
ACCESSION CB565888  
VERSION CB565888.1 GI:29485418  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 895)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-x@mail.nih.gov  
Tissue Procurement: Guthrie cDNA Resource Center  
CDNA Library Preparation: Guthrie cDNA Resource Center  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
Plate: IRBF001 row: f column: 09  
High quality sequence stop: 763.  
Location/Qualifiers  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6519213"  
/tissue\_type="mixed"  
/lab\_host="DH10B (TI-phage-resistant)"  
/clone\_lib="NIH\_MGC\_146"  
/notes="Vector: pCDNA3.1; Site 1: multiple; Site 2: multiple; ORF's were PCR-amplified (from IMAGE Clones or from commercially available cDNA libraries) and cloned by the Guthrie cDNA Resource Center (www.guthrie.org/cdna) into pCDNA3.1. For specific information on cloning sites (which vary by clone), please refer to the Guthrie website, using the Guthrie ID given in the file ftp://image.llnl.gov/image-rearrayed\_plates/IRBF.presv.dat a. Note: this is a NIH\_MGC Library."

FEATURES  
source

1. .895  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/tissue\_type="mixed"  
/lab\_host="DH10B (TI-phage-resistant)"  
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/notes="Vector: pCDNA3.1; Site 1: multiple; Site 2: multiple; ORF's were PCR-amplified (from IMAGE Clones or from commercially available cDNA libraries) and cloned by the Guthrie cDNA Resource Center (www.guthrie.org/cdna) into pCDNA3.1. For specific information on cloning sites (which vary by clone), please refer to the Guthrie website, using the Guthrie ID given in the file ftp://image.llnl.gov/image-rearrayed\_plates/IRBF.presv.dat a. Note: this is a NIH\_MGC Library."

ORIGIN

Query Match		69.6%; Score 803.6; DB 6; Length 895;
Best Local Similarity		97.0%; Pred. No. 4.5e-200;
Matches		840; Conservative 0; Mismatches 24; Indels 2; Gaps 2;
QY	1	ATGGACTCCCGATCCAGATCTTCCGGGGAGCGCGGCTTACCTGGCGCCGAGCGGC 60
DB	2	ATGGAATCCCGATCCAGATCTTCCGGGGAGCGCGGCTTACCTGGCGCCGAGCGGC 61
QY	61	TGCTGCCCGCCCAACAGCAGCGCTTCCGGCTTCCGGCTGGCGGAGCCGACAGCAACGCG 120
DB	62	TGCTGCCCGCCCAACAGCAGCGCTTCCGGCTTCCGGCTGGCGGAGCCGACAGCAACGCG 121
QY	121	AGCGCGGCTCGAGGACGCGCAGCTGAGCGCGCGCACATCTCCCGCGCCATCCCGGTC 180
DB	122	AGCGCGGCTCGAGGACGCGCAGCTGAGCGCGCGCACATCTCCCGCGCCATCCCGGTC 181
QY	181	ATCATCAGCGCGTCTACTCCGAGTGTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 240
DB	182	ATCATCAGCGCGTCTACTCCGAGTGTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 241
QY	241	ATGTCGTGATCATCCGATACACAGATGACAGCAACCAACCAATTTACATATTATAC 300
DB	242	ATGTCGTGATCATCCGATACACAGATGACAGCAACCAACCAATTTACATATTATAC 301
QY	301	CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCCAGAGTACGGTCTACTTG 360
DB	302	CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCCAGAGTACGGTCTACTTG 361
QY	361	ATGAATTCCTGGCTTTGGGAGTGTCTGTGCAAGATGATTAATTTCCATTTGATTAATAC 420
DB	362	ATGAATTCCTGGCTTTGGGAGTGTCTGTGCAAGATGATTAATTTCCATTTGATTAATAC 421
QY	421	ACATGTTTACCAAGATCTTACCTTTGACATGATGAGCGTGGACCGCTACATTTGCCGTC 480
DB	422	ACATGTTTACCAAGATCTTACCTTTGACATGATGAGCGTGGACCGCTACATTTGCCGTC 481
QY	481	TGCCACCCCGTGAAGCTTTGGACTTCCGACACACCTTTGAAGCAAGATCATCAATATC 540
DB	482	TGCCACCCCGTGAAGCTTTGGACTTCCGACACACCTTTGAAGCAAGATCATCAATATC 541
QY	541	TGATCTGGCTGTCTGTCATCTGTGTCATCTGTGTCATCTGTGTCATCTGTGTCATCTGT 600
DB	542	TGATCTGGCTGTCTGTCATCTGTGTCATCTGTGTCATCTGTGTCATCTGTGTCATCTGT 601
QY	601	GTGAGGAGACGTCGATGTCATGAGTGTCTGTCATGAGTGTCTGTCATGAGTGTCTGTC 660
DB	602	GTGAGGAGACGTCGATGTCATGAGTGTCTGTCATGAGTGTCTGTCATGAGTGTCTGTC 661
QY	661	TGCTGGGACCTCTTCAATGAAGATCTGCTGCTTTCATCTTTGCTTCTGTCATCTGTCCTC 720
DB	662	TGCTGGGACCTCTTCAATGAAGATCTGCTGCTTTCATCTTTGCTTCTGTCATCTGTCCTC 721
QY	721	ATCATCATGTCGTACACCTGATGATCTGTCGTCCTCAAGAGCGTCC-GGCTCTCTTTC 779
DB	722	ATCATCATGTCGTACACCTGATGATCTGTCGTCCTCAAGAGCGTCCGCTCTCTTTC 781
QY	780	TGCTCCCGAGAGAGATC-GCAACCTGGTAGATCACCAGCTGCTGCTGCTGCTGCTGCTG 838
DB	782	TGCTCCCGAGAGAGATCNGCACCCTGCTAGGATCACCAGCTGCTGCTGCTGCTGCTGCTG 841
QY	839	TGCGAGTCTTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 864
DB	842	GTGGCGAGTCTTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 867
RESULT 2		
LOCUS		CO960667
DEFINITION		AGENCOURT 30842630 NIH_MGC_146 Homo sapiens cDNA clone
ACCESSION		IMAGE:7389810 5', mRNA sequence.
VERSION		CO960667
KEYWORDS		CO960667.1 GI:51325223 EST.

SOURCE		Homo sapiens (human)
ORGANISM		Homo sapiens
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS		1 (bases 1 to 762)
TITLE		NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL		National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT		Unpublished (1999)
		Contact: Daniela S. Gerhard, Ph.D.
		Office of Cancer Genomics
		National Cancer Institute / NIH
		Bldg. 31 Rm10A07 Bethesda, MD 20892
		Email: cgabbs-remail.nih.gov
		Tissue Procurement: Guthrie cDNA Resource Center
		cDNA Library Preparation: Guthrie cDNA Resource Center
		CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
		DNA Sequencing by: Agencourt Bioscience Corporation
		Clone Distribution: MGC clone distribution information can be
		found through the I.M.A.G.E. Consortium/LLNL at:
		http://image.llnl.gov
		Plate: IRB18 row: d column: 04
		High quality sequence start: 30
		High quality sequence stop: 549.
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		/note="Vector: pCDNA3.1; Site 1: multiple; Site 2: multiple; ORF's were PCR-amplified (from IMAGE Clones or from commercially available cDNA libraries) and cloned by the Guthrie cDNA Resource Center (www.guthrie.org/cDNA) into pCDNA3.1. For specific information on cloning sites (which vary by clone), please refer to the Guthrie website, using the Guthrie ID given in the file ftp://image.llnl.gov/image.rearrayed_plates/IRBF.presv.dat a. Note: this is a NIH_MGC Library."
ORIGIN		
		Query Match 50.4%; Score 581.8; DB 7; Length 762;
		Best Local Similarity 97.1%; Pred. No. 9.7e-142;
		Matches 603; Conservative 0; Mismatches 17; Indels 1; Gaps 1;
QY	1	ATGGACTCCCGATCCAGATCTTCCGGGGAGCGCGGCTTACCTGGCGCCGAGCGGC 60
DB	27	ATGGAATCCCGATCCAGATCTTCCGGGGAGCGCGGCTTACCTGGCGCCGAGCGGC 86
QY	61	TGCTGCCCGCCCAACAGCAGCGCTTCCGGCTTCCGGCTGGCGGAGCCGACAGCAACGCG 120
DB	87	TGCTGCCCGCCCAACAGCAGCGCTTCCGGCTTCCGGCTGGCGGAGCCGACAGCAACGCG 146
QY	121	AGCGCGGCTCGAGGACGCGCAGCTGGAGCGCGGCACATCTCCCGCGCCATCCCGGTC 180
DB	147	AGCGCGGCTCGAGGACGCGCAGCTGGAGCGCGGCACATCTCCCGCGCCATCCCGGTC 206
QY	181	ATCATCAGCGCGTCTACTCCGAGTGTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 240
DB	207	ATCATCAGCGCGTCTACTCCGAGTGTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 266
QY	241	ATGTCGTGATCATCCGATACACAGATGACAGCAACCAACCAATTTACATATTATAC 300
DB	267	ATGTCGTGATCATCCGATACACAGATGACAGCAACCAACCAATTTACATATTATAC 326
QY	301	CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCCAGAGTACGGTCTACTTG 360
DB	327	CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTCCAGAGTACGGTCTACTTG 386
QY	361	ATGAATTCCTGGCTTTGGGAGTGTCTGTGCAAGATGATTAATTTCCATTTGATTAATAC 420

Db 387 ATGAATTCCTGGCCCTTTGGGATGCTGCTGCAAGATAGTAATTTCAATTGATTACTAC 446  
 Qy 421 AACATGTTTACCAGCATCTTCACTTGAACCATGATGAGCGTGGACCGCTACATTGCCGTG 480  
 Db 447 AACATGTTTACCAGCATCTTCACTTGAACCATGATGAGCGTGGACCGCTACATTGCCGTG 506  
 Qy 481 TGCACCCCGTGAAGGCTTTGGACTTCGCGACACCTTTGAAGGCAAGATCATCAATATC 540  
 Db 507 TGCACCCCGTGAAGGCTTTGGACTTCGCGACACCTTTGAAGGCAAGATCATCAATATC 566  
 Qy 541 TGCATCTGGCT-GCTGCTGATCTGTTGGCATCTCTGCAATAGTCCCTTGGAGGCCAA 599  
 Db 567 TGCATCTGGCTGGCTGCTGATCTCTGTTAGCATCTCTGTAATATCTCTTGGGAGCGCAA 626  
 Qy 600 AGTCAGGGAAGACGTCGATGT 620  
 Db 627 AATCAGGGAAGACTCGAGGT 647

RESULT 3  
 CO960682/c  
 LOCUS  
 DEFINITION AGENCOURT 30842262 NIH\_MGC\_146 Homo sapiens cDNA clone  
 IMAGE:7389810 3', mRNA sequence.

ACCESSION CO960682.1 GI:51325238  
 VERSION EST.  
 KEYWORDS  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS NIH-MGC http://mgi.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-remail.nih.gov

Tissue Procurement: Guthrie cDNA Resource Center

cDNA Library Preparation: Guthrie cDNA Resource Center

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: IRB18 row: d column: 04

High quality sequence start: 214

High quality sequence stop: 494.

Location/Qualifiers

1..784

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/mol\_type="mRNA"

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/note="vector: pcDNA3.1; Site 1: multiple; Site 2:

multiple; ORF's were PCR-amplified (from IMAGE clones or

from commercially available cDNA libraries) and cloned by

the Guthrie cDNA Resource Center (www.guthrie.org/cDNA)

into pcDNA3.1. For specific information on cloning sites

(which vary by clone), please refer to the Guthrie

website, using the Guthrie ID given in the file

ftp://image.llnl.gov/image/rearrayed\_plates/IRB18.presv.dat

a. Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 45.0%; Score 518.8; DB 7; Length 784;

Best Local Similarity 97.6%; Pred. No. 3.7e-125;

Matches 537; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Qy 586 CTTGGAGCCACCAAGTCAGGAGAGCGTGGATGCTCATTTGAGTCTCTTTCAGTTCCTCA 645  
 Db 577 CTTTGGAGCCACCAAGTCA-GGAAGAGCGTGGATGCTCATTTGAGTCTCTTTCAGTTCCTCA 519  
 Qy 646 GATGATGACTACTCTCTGGTGGGACCTCTTATGAAGATCTGGGCTTCATCTTTGCCCTTC 705  
 Db 518 GATGATGACTACTCTCTGGTGGGACCTCTTATGAAGATCTGGGCTTCATCTTTGCCCTTC 459  
 Qy 706 GTGATCCCTGCTCCTCATCATCATCTGCTTACACCTGATGATCTCGCTCTCAAGAGC 765  
 Db 458 GTGATCCCTGCTCCTCATCATCATCTGCTTACACCTGATGATCTCGCTCTCAAGAGC 399  
 Qy 766 GTCCGGCTCCTTTCTGGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTG 825  
 Db 398 GTCCGGCTCCTTTCTGGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTG 339  
 Qy 826 GTCTGTGTGGTGGGAGTCTTCTGTTGCTGTCTGGACTCCCATTCATATTCATCTG 885  
 Db 338 GTCTGTGTGGTGGGAGTCTTCTGCTGTCTGTCTGCTGCTCTCTCAGTATTCATCTG 279  
 Qy 886 GTGGAGGCTCTGGGGAGCACCTCCACAGCACAGCTGCTCTCCAGTATTCATCTG 945  
 Db 278 GTGGAGGCTCTGGGGAGCACCTCCACAGCACAGCTGCTCTCTCAGTATTCATCTG 219  
 Qy 946 ATCGCCTTAGGCTATACCAACAGTAGGCTGTAATCCCATTTCTCTACGCTTTCTTTGATGAA 1005  
 Db 218 ATCGCCTTAGGCTATACCAACAGTAGGCTGTAATCCCATTTCTTACGCTTTCTCGATGAA 159  
 Qy 1006 AACTTCAAGCGGTGTTTCCGGGACTTCTGTTTCCACTGAAGATGAGAGCGGCGAG 1065  
 Db 158 GACTTCAAGCGGTGTTTCCGGGACTTCTGCTTTTCACTGAAGATGAGAGCGGCGAG 99  
 Qy 1066 AGCACTAGCAGAGTCGGAATACAGATTCAGATCTCTTACCTAGGAGGACATCGATGG 1125  
 Db 98 AGCACTAGCAGAGTCGGAATACAGATTCAGATCTCTTACCTAGGAGGACATCGATGG 39  
 Qy 1126 ATGAATAAAC 1135  
 Db 38 ATGATGAACC 29

RESULT 4

CF593603

LOCUS

DEFINITION

AGENCOURT 15623822 NIH\_MGC\_147 Homo sapiens cDNA clone

IMAGE:30531690 5', mRNA sequence.

ACCESSION CF593603

VERSION CF593603.1 GI:36347316

KEYWORDS EST.

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 837)

AUTHORS

NIH-MGC http://mgi.nci.nih.gov/.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Stefan Hanson

cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help

and advice from Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: NDAMG22 row: n column: 19

High quality sequence stop: 592.

[illegible]













[illegible]

JOURNAL REFERENCE AUTHORS	Nature 409, 685-690 (2001)	Qy	315	TGCTTTAGTTACTACAAACCATGCCCTTTACAGAGTACGGTCTTACCTTGATGAATTCCTGGCC	374
TITLE	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.	Db	483	TACCTGGTCTGCTGACACTGCCCTTCCAGGGCAGACACATCTTCTGGGCTTCTGGCC	542
JOURNAL REFERENCE AUTHORS	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002) 6 (bases 1 to 2940)	Qy	375	TTTTGGGATGTGCTGTGCAAGATAGTAATTTTCATTGATTAACAACATGTTTCAACAG	434
		Db	543	ATTTGGGAATGCACTGTGCAAGACGGTCAATGCTATCGACTACTACAACATGTTTACCAG	602
		Qy	435	CATCTTCACCTTGACCATGATGAGCGGTGAGCCGTACATGCGGTGTCACCCCGTGA	494
		Db	603	CACCTTCACCTTGACCTGCCATGAGTGTAGACCGTATGTAGCTATCTGCCACCTATCCG	662
		Qy	495	GGCTTTGGACCTTCGCGCACACCTTTGAAGGCAAAAGATCATCAATATCTGCATCTGGCTCT	554
		Db	663	TGCCCTTGATGTTTGGACATCCAGTAAAGCCAGCCGTTAATGTGGCCATATGGCCCT	722
		Qy	555	GTCTGTATCTGTTGGCATCTCTGCAATAGTCTTTGGAGGACCAAAAGTCAAGGAGAGCT	614
		Db	723	GGCTTCGGTGGTGGTGTCTCTGTTGCCATCATGGGCTCAGCACAAAGT-----GGAGGA	776
		Qy	615	CGATGTCTATTGAGTGTCTTGCAGTTCACAGATGATGACTACTCTCTGGTGGGACCTCTT	674
		Db	777	TGAAGAGATCGAGTGCCTGTGGAGATCCCGCCCTCAGGA---CTATTGGGGCCCTGT	833
		Qy	675	CATGAAGATCTGCTCTTTCATCTTTGCTTGTGATCCCTGTCTCTCATCATCATCTGCTG	734
		Db	834	ATTGGCATCTGCACTTCTCTTTTCTTCATCATCCGGTCTGTGATCATCTCTGCTG	893
		Qy	735	CTACACCTGATGATCTGCTGTCTCAAGAGCGTCCGGCTCTTTTGTGGTCCCGAGAGAA	794
		Db	894	CTACAGCCTCATGATTCGACGACTTCGTGGTGTCCGGCTGCTTTTCAGGCTCCCGAGAA	953
		Qy	795	AGATCGCAACCTGGTAGGATCACCAGACTGCTCTGGTGGTGGTGGTGGTGGTGGTGGT	854
		Db	954	GGACCGGAACCTGGACGACATCACACGGCTGGTACTGGTAGTGTGGTGTGGTGTGGG	1013
		Qy	855	CTGCTGGACTCCCATTCACATATTCATCTCTGGTGGAGGCTCTGGGGAGCACCTCCACAG	914
		Db	1014	CTGCTGGACACTGTGAGGCTCTTTGCTGGTTCAGGACTGGGTGTTCAGCCAGGTAG	1073
		Qy	915	CACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCTTAGGCTTATACCAACAGTAGCCT	974
		Db	1074	TGAGACTGCACTAGTACCATCTCTGCGCTTCTGCACAGCCCTGGGCTATGTCAACAGTGTCT	1133
		Qy	975	GAATCCCATCTCTACGCCCTTCTTGATGAAACTTCAAGCGGTGTTTCCGGGACTTCTG	1034
		Db	1134	CAATCCCATCTCTATGCTTTCTTGGATGAGAACTTCAAGGCCCTGCTTTAGAAAAGTCTG	1193
		Qy	1035	CTTTCACCTGAAGATGAGGTGGAGCGGAGACACTAGCAGAGTCCGAAATACAGTTCA	1094
		Db	1194	CTGTGCTTTCGCCCTGCACCGGAGATGCAGGTTCTTGATGCTGTGGCAGCATTGCCAA	1253
		Qy	1095	GGAT 1098	
		Db	1254	GGAT 1257	
RESULT 12					
AK043275					
LOCUS					
DEFINITION	AK043275 2974 bp mRNA linear HTC 03-APR-2004 Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730079L19 product:NOICETPIN RECEPTOR (ORPHANIN FQ RECEPTOR), full insert sequence.				
ACCESSION	AK043275				
VERSION	AK043275.1 GI:26089596				
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	1 Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	Carninci, P. and Hayashizaki, Y.				
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: <a href="http://genome.gsc.riken.jp/">http://genome.gsc.riken.jp/</a> URL: <a href="http://fantom.gsc.riken.jp/">http://fantom.gsc.riken.jp/</a>				
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Qy	214	GTGGGCTTGTGGGCAACTCGCTGGTCAATGTTCTGATCAT-----	254		
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Qy	255	CCGATACACAAGATGAAGACAGCAACCAATTTACATTTAACTGGCTTTGGCAGA	314		
Db	423	CAGGCACACCAAGATGAAGACTGTCTACCAACATTTACATTTAATCTGGCACTGGCTGA	482		

```

TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 9279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci, P., Shibata, Y., Hayateu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
MEDLINE 11076861
PUBMED 11076861
REFERENCE 5
AUTHORS The PANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
MEDLINE 120530913
PUBMED 120530913
REFERENCE 6
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayaishida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
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Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akaira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/.
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 REFERENCE  
 1  
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes  
 Genome Res. 10 (10), 1617-1630 (2000)  
 20499374  
 11042159

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 REFERENCE  
 3  
 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
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 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer  
 Genome Res. 10 (11), 1757-1771 (2000)  
 20530913  
 11076861

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 REFERENCE  
 4  
 The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 Functional annotation of a full-length mouse cDNA collection  
 Nature 409, 685-690 (2001)

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 REFERENCE  
 5  
 The FANTOM Consortium and the RIKEN Genome Exploration Research  
 Group Phase I & II Team.  
 Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
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 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
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 Muramatsu, M. and Hayashizaki, Y.  
 Direct Submission

TITLE  
 JOURNAL  
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome

COMMENT  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
 Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.jp,  
 URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,  
 Fax: 81-45-503-9216]  
 cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Please visit our web site for further details.  
 URL: http://genome.gsc.riken.jp/  
 URL: http://fantom.gsc.riken.jp/.

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VERSION AY410747.1 GI:39766715
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AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 879)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
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VERSION AL283934
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Tetraodonidae; Tetraodontidae; Tetraodon.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
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Tetraodontidae; Tetraodon.

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**AUTHORS** Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.  
**TITLE** Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence  
**JOURNAL** Nat. Genet. 25 (2), 235-238 (2000)  
**MEDLINE** 20296833  
**PUBMED** 10835645  
**REFERENCE** 2  
**AUTHORS** Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C., Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.  
**TITLE** Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis  
**JOURNAL** Genome Res. 10 (7), 939-949 (2000)  
**MEDLINE** 20359837  
**PUBMED** 10899143  
**REFERENCE** 3 (bases 1 to 1053)  
**AUTHORS** Genoscope.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : secref@genoscope.cns.fr - Web : www.genoscope.cns.fr)  
**COMMENT** This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/tetraodon.  
**FEATURES** Location/Qualifiers  
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**ORIGIN**

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 Matches 587; Conservative 8; Mismatches 230; Indels 74; Gaps 7;

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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8: gb_pl.*	
9: gb_pr.*	
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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20 914 79.2 4742 10 RNU00442  
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LOCUS Human kappa opioid receptor (hKOR) mRNA, complete cds.  
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ACCESSION U17298  
VERSION U17298.1 GI:596069  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
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Simonin,F., Gaveriaux-Ruff,C., Befort,K., Matthes,H., Lannes,B., Micheletti,G., Mattei,M.G., Charron,G., Bloch,B. and Kieffer,B. kappa-Opioid receptor in humans: cDNA and genomic cloning, B. chromosomal assignment, functional expression, pharmacology, and expression pattern in the central nervous system  
Proc. Natl. Acad. Sci. U.S.A. 92 (15), 7006-7010 (1995)  
JOURNAL MEDLINE 95350200  
PUBMED 7624359  
REFERENCE 2 (bases 1 to 1154)  
Mansson,B., Bare,L. and Yang,D. Isolation of a human kappa opioid receptor cDNA from placenta  
Biochem. Biophys. Res. Commun. 202 (3), 1431-1437 (1994)  
JOURNAL MEDLINE 94338360  
PUBMED 8060324  
REFERENCE 3 (bases 1 to 1154)  
Kieffer,B. Direct Submission  
Submitted (18-NOV-1994) Brigitte Kieffer, Ecole Supérieure De Biotechnologie De Strasbourg, Boulevard Sebastien Brandt, Illkirch, 67400, France  
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Best Local Similarity 99.9%; Pred. No. 9.9e-202;
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AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
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thereof
JOURNAL Patent: WO 02068579-A 9091 06-SEP-2002;
PE Corporation (NY) (US)
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Matches 1153; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Best Local Similarity	99.9%; Pred. No. 9.9e-202;
Matches 1153; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
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QY	241 ATGTTCTGTATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300
Db	618 ATGTTCTGTATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 677
QY	301 CTGGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCCCTTTTCAGAGTACGGTCTACTTG 360
Db	678 CTGGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCCCTTTTCAGAGTACGGTCTACTTG 737
QY	361 ATGAATTCCTGGCTTTTGGGATGTCTGTGCAAGTACTAATTTCCATTGATTACTAC 420
Db	738 ATGAATTCCTGGCTTTTGGGATGTCTGTGCAAGTACTAATTTCCATTGATTACTAC 797

421 AACATCTTCCACGAGCATCTTCCATCTGACCATGAGCGTGACCGCTACATTTGCCGNG 480  
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RESULT 4  
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 LOCUS AR270854 1182 bp DNA linear PAT 10-APR-2003  
 DEFINITION Sequence 1417 from patent US 6500938.  
 ACCESSION AR270854  
 VERSION AR270854.1 GI:29702088  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.  
 1 (bases 1 to 1182)  
 Au-Young, J. and Seilhamer, J. J.  
 TITLE Composition for the detection of signaling pathway gene expression  
 JOURNAL Patent: US 6500938-A 1417 31-DEC-2002;  
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 1..1182  
 /organism="unknown"  
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Query Match 99.2%; Score 1144.4; DB 6; Length 1182;  
 Best Local Similarity 99.5%; Pred. No. 2.9e-200;  
 Matches 1148; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 1 ATGGACTCCCGATCCAGATCTTCCGCGGAGCGGGCCCTTACTCTGCGCCCGAGCGCC 60  
 14 ATGGAATCCCGATTCAGATCTTCCGCGGAGCGGGCCCTTACTCTGCGCCCGAGCGCC 73  
 61 TGCCTGCCCGCCACAGCAGCGCGCTGGTTCCCGCTGGGCGGAGCCCGAGCAGCAACCGC 120  
 74 TGCCTGCCCGCCACAGCAGCGCGCTGGTTCCCGCTGGGCGGAGCCCGAGCAGCAACCGC 133  
 121 AGCGCGGCTCGAGGAGCGCGCAGCTGAGCGCGCGCACATCTCCCGCGCCATCCCGGTC 180  
 134 AGCGCGGCTCGAGGAGCGCGCAGCTGAGCGCGCGCACATCTCCCGCGCCATCCCGGTC 193  
 181 APTCATCAGCGGCTCTACTCCGTAGTGTTCGTGGGCTTGGTGGGCAACTCGCTGTGTC 240  
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 614 GTCAGGAGAGAGTGTGATGTCATCTGTCAGTCTCTTCCAGATGATGACTACTACTCC 673  
 661 TGTGTGGGACCTCTTTCATGAAGATCTGCGTCTTTCATCTTTGCTTCTGATGCTGCTGCTC 720  
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RESULT 5  
LOCUS AX548862 1182 bp DNA linear PAT 26-NOV-2002  
DEFINITION Sequence 147 from Patent WO02061087.  
ACCESSION AX548862  
VERSION AX548862.1 GI:25813740  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE  
AUTHORS Burmer,G.C., Roush,C.L. and Brown,J.P.  
TITLE Antigenic peptides, such as for G protein-coupled receptors (GPCRs), antibodies thereto, and systems for identifying such antigenic peptides  
JOURNAL Patent: WO 02061087-A 147 08-AUG-2002;  
Lifespan Biosciences, Inc. (US)  
FEATURES  
source Location/Qualifiers  
1. .1182  
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ORIGIN  
Query Match 99.2%; Score 1144.4; DB 6; Length 1182;  
Best Local Similarity 99.5%; Pred. NO. 2.9e-200;  
Matches 1148; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGGACTCCCGATCCAGATCTTCGGGGGAGCGGGCCCTACTGCGGCCCGAGCGCC 60  
Db 14 ATGGAATCCCGATTCAGATCTTCGGGGGAGCGCTGCGCCCTACTGCGGCCCGAGCGCC 73  
Qy 61 TGCCTGCCCGCCCAACAGCAGCGCTGTTTCCCGCTGGCGCGAGCCCGACAGCAACGCG 120  
Db 74 TGCCTGCCCGCCCAACAGCAGCGCTGTTTCCCGCTGGCGCGAGCCCGACAGCAACGCG 133  
Qy 121 AGCGCGGCTCGGAGGAGCGCAGCTGGAGCGCGCGCACATCTCCCGGCCATCCCGGTC 180  
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Qy 541 TGCATCTGGCTGCTGCTGCTCATCTGTTGGGATCTCTGCAATAGTCTTGGAGGACCCAAA 600  
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Db 734 ATCATCATCTGCTGTACACCCCTGATGATCTGCTGCTCTCAAGAGCGTCCGCTCTTCT 793  
Qy 781 GGCTCCCGAGAAAGATCGCAACCTCGTAGGATCACAGACTGGTCTCTGCTGGTGGTG 840  
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RESULT 6  
AX774764 1182 bp DNA linear PAT 09-JUL-2003  
LOCUS AX774764  
DEFINITION Sequence 80 from Patent WO03038129.  
ACCESSION AX774764  
VERSION AX774764.1 GI:32486280  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
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REFERENCE  
AUTHORS Raponi,M.  
TITLE Methods for assessing and treating leukemia  
JOURNAL Patent: WO 03038129-A 80 08-MAY-2003;  
Ortho-Clinical Diagnostics, Inc. (US)  
FEATURES  
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Query Match 99.2%; Score 1144.4; DB 6; Length 1182;



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QY	1	ATGGACTCCCGATCCAGATCTTCCGCGGGAGCGCGGCTTACCTGCGCGCCCGAGCGCC	60
Db	14	ATGGAATCCCGATTCCAGATCTTCCGCGGGAGCTTGGCCCTACCTTGCGCCCGAGCGCC	73
QY	61	TGCTCGCGCCCAACAGCAGCGCTCGTTTCCGGCTGGCGGAGCCCGACAGCAACGGC	120
Db	74	TGCTCGCGCCCAACAGCAGCGCTCGTTTCCGGCTGGCGGAGCCCGACAGCAACGGC	133
QY	121	AGCGCGGCTCGAGGAGCGCGAGCTGGAGCCCGGACATCTTCCCGGCGCATCCCGGTC	180
Db	134	AGCGCGGCTCGAGGAGCGCGAGCTGGAGCCCGGACATCTTCCCGGCGCATCCCGGTC	193
QY	181	ATCATCAGCGCGTCTACTCCGAGTGTTCGTCGGCTGGTGGGCAACTCGCTGGTC	240
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QY	301	CTGGCTTTGGCAGATGCTTTAGTTACTCAACCATGCCCTTTCCAGAGTACGGTCTACTTG	360
Db	314	CTGGCTTTGGCAGATGCTTTAGTTACTCAACCATGCCCTTTCCAGAGTACGGTCTACTTG	373
QY	361	ATGAATTCCTGGCTTTGGGATGTCTGCAAGATAGTAAATTTCCATTTGATTTACTAC	420
Db	374	ATGAATTCCTGGCTTTGGGATGTCTGCAAGATAGTAAATTTCCATTTGATTTACTAC	433
QY	421	AACATGTTACACAGATCTTCACTTGACCATGAGCGTGACCGCTACATTTGCCGTG	480
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QY	541	TGCATCTGGCTGTCTGCTCATCTGTGGCATCTCTGCATAGTCTTGGAGGACCAAA	600
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Db	614	GTAGGGAAGACGCTCGATGTCATTGAGTGTCTCTGAGTTCCTCCAGATGATGACTACTC	673
QY	661	TGTTGGGACCTCTTTCATGAAGATCTGGCTTTCATCTTTGCTTTCGTTGATCCCTGCTTC	720
Db	674	TGTTGGGACCTCTTTCATGAAGATCTGGCTTTCATCTTTGCTTTCGTTGATCCCTGCTTC	733
QY	721	ATCATCATCTGCTGTACACCTCGATGATCTCGCTCTCAAGAGCGTCCGGCTCCTTTCT	780
Db	734	ATCATCATCTGCTGTACACCTCGATGATCTCGCTCTCAAGAGCGTCCGGCTCCTTTCT	793
QY	781	GGCTCCCGAGAGAAAGATCGCAACTCGTAGGATCACAGACTGTCTGTGGTGGTG	840
Db	794	GGCTCCCGAGAGAAAGATCGCAACTCGTAGGATCACAGACTGTCTGTGGTGGTG	853
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QY	901	AGACCTCCCAACAGCAGCTGTCTCTCCAGCTATTACTTCTGCTGCTTGGCTAT	960
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QY	961	ACCAACAGTAGGCTGAATCCCATTTCTACGCCCTTTCTTGATGAAATCTTCAAGCGGTGT	1020
Db	974	ACCAACAGTAGGCTGAATCCCATTTCTACGCCCTTTCTTGATGAAATCTTCAAGCGGTGT	1033
QY	1021	TTCCGGGACTTCTGCTTTCCATGAAGATGAGGATGGAGCGGCGAGCACTTACAGATC	1080
Db	1034	TTCCGGGACTTCTGCTTTCCATGAAGATGAGGATGGAGCGGCGAGCACTTACAGATC	1093
QY	1081	CGAAATACAGTTCCAGATCTTACCTGAGGACATCGATGGATGAATAAACAGTA	1140
Db	1094	CGAAATACAGTTCCAGATCTTACCTGAGGACATCGATGGATGAATAAACAGTA	1153
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Query Match 99.2%; Score 1144.4; DB 9; Length 1182;			
Best Local Similarity 99.5%; Pred. No. 2.9e-200;			
Matches 1148; Conservative 0; Mismatches 6; Indels 0; Gaps 0;			
QY	1	ATGGACTCCCGATCCAGATCTTCCGCGGGAGCGCGGCTTACCTGCGCGCCCGAGCGCC	60
Db	14	ATGGAATCCCGATTCCAGATCTTCCGCGGGAGCTTGGCCCTACCTTGCGCCCGAGCGCC	73
QY	61	TGCTCGCGCCCAACAGCAGCGCTCGTTTCCGGCTGGCGGAGCCCGACAGCAACGGC	120
Db	74	TGCTCGCGCCCAACAGCAGCGCTCGTTTCCGGCTGGCGGAGCCCGACAGCAACGGC	133
QY	121	AGCGCGGCTCGAGGAGCGCGAGCTGGAGCCCGGACATCTTCCCGGCGCATCCCGGTC	180
Db	134	AGCGCGGCTCGAGGAGCGCGAGCTGGAGCCCGGACATCTTCCCGGCGCATCCCGGTC	193

Qy	181	ATCATCAGCGCGGTCTACTCGTAGTGTTTGGTGGCGGTGGTGGGCAATCGCGTGGTC	240
Db	194	ATCATCAGCGCGGTCTACTCGTAGTGTTTGGTGGCGGTGGTGGGCAATCGCGTGGTC	253
Qy	241	ATGTTTGGTGATCATCCGATACACAAAGATGAAGCAGCAACCAATTTTACATATTTAAAC	300
Db	254	ATGTTTGGTGATCATCCGATACACAAAGATGAAGCAGCAACCAATTTTACATATTTAAAC	313
Qy	301	CTGGCTTTGGCAGATGCTTTTAGTTAGTTACTACAAACCATGCGCTTTACAGTAGCGGTCTACTTTG	360
Db	314	CTGGCTTTGGCAGATGCTTTTAGTTAGTTACTACAAACCATGCGCTTTACAGTAGCGGTCTACTTTG	373
Qy	361	ATGAATTCCTGCGCTTTTGGGGATGCTGTCGAAGATAGTAATTTTCCATTTGATTACTAC	420
Db	374	ATGAATTCCTGCGCTTTTGGGGATGCTGTCGAAGATAGTAATTTTCCATTTGATTACTAC	433
Qy	421	AACATGTTTACCAGCATCTTTCACCTTGACCATGATGAGCGTGGACCGCTACATTTGCCGCTG	480
Db	434	AACATGTTTACCAGCATCTTTCACCTTGACCATGATGAGCGTGGACCGCTACATTTGCCGCTG	493
Qy	481	TGCACACCCGTTGAAGCTTTGGACTTTCGCAACACCCTTGAAGGCAAAAGATCATCAATATC	540
Db	494	TGCACACCCGTTGAAGCTTTGGACTTTCGCGCAACCCCTTGAAGGCAAAAGATCATCAATATC	553
Qy	541	TGCATCTGGCTGCTGCTGCTCATCTGTTGGCATCTCTGCAATAGTTCCTTGGAGGACCCAAA	600
Db	554	TGCATCTGGCTGCTGCTGCTCATCTGTTGGCATCTCTGCAATAGTTCCTTGGAGGACCCAAA	613
Qy	601	GTCAAGGGAAGACGTGCGATGTCATTGAGTGTCTTTCGAGTTCCTCCAGATGATGACTACTCC	660
Db	614	GTCAAGGGAAGACGTGCGATGTCATTGAGTGTCTTTCGAGTTCCTCCAGATGATGACTACTCC	673
Qy	661	TGGTGGGACCTCTTTCATGAAGATCTGCGTCTTTCATCTTTTGGCTTCGTGATCCCTGTCTCT	720
Db	674	TGGTGGGACCTCTTTCATGAAGATCTGCGTCTTTCATCTTTTGGCTTCGTGATCCCTGTCTCT	733
Qy	721	ATCATCATCTGCTGCTCACACCTCATGATCTCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT	780
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Qy	781	GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACAGACTGGTCTCTGGTGGTGGTG	840
Db	794	GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACAGACTGGTCTCTGGTGGTGGTG	853
Qy	841	GCAGTCTTTCGTCGTCGTGCACTCCCATTCACATATTCATCTCTGGTGGAGGCTCTGGGG	900
Db	854	GCAGTCTTTCGTCGTCGTGCACTCCCATTCACATATTCATCTCTGGTGGAGGCTCTGGGG	913
Qy	901	AGCACCTCCCAACAGCAGCTGCTCTCTCCAGCTATTACTTCTGCATTCCTTAGGCTAT	960
Db	914	AGCACCTCCCAACAGCAGCTGCTCTCTCCAGCTATTACTTCTGCATTCCTTAGGCTAT	973
Qy	961	ACCAACAGTAGCCGTAATCCCATTTCTCTACGCCCTTTCTTGATGAAAACTTCAAGCGGTGT	1020
Db	974	ACCAACAGTAGCCGTAATCCCATTTCTCTACGCCCTTTCTTGATGAAAACTTCAAGCGGTGT	1033
Qy	1021	TTCCGGGACTTCTGCTTTTCCACTGAAGTAGGATGGAGCGGCAGAGCACTAGCAGATC	1080
Db	1034	TTCCGGGACTTCTGCTTTTCCACTGAAGTAGGATGGAGCGGCAGAGCACTAGCAGATC	1093
Qy	1081	CGAAATACAGTTCAGGATCTCTGCTTTTACTGAGGGACATCGATGGATGAAATAAACACAGTA	1140
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Qy	1141	TGACTAGTCGTGGA	1154
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RECIT. T. 8

AR281679

## LOCUS

DNA

linear

PAT 10-APR-2003

DEFINITION Sequence 1 from patent US 6518480.

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ACCESSION	AR281679	AR281679.1	GI:29717434	
VERSION				
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 1143)			
TITLE	Conklin,B.R.			
JOURNAL	Selective targeted cell activation by expression of a G			
FEATURES	protein-coupled receptor activated superiorly by synthetic ligand			
source	Patent: US 6518480-A 1 11-FEB-2003;			
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Db	61	TGCGTGGCCCCCAACAGCAGCGCCTGGTTTCCGGTGGCGCGAGCCGACGACCAACGGC	120	
Qy	121	AGCGCGGCTCGAGAGCGGAGCTGGAGCCCGCGCACATCTCCCGGCCCATCCCGGTC	180	
Db	121	AGCGCGGCTCGAGAGCGGAGCTGGAGCCCGCGCACATCTCCCGGCCCATCCCGGTC	180	
Qy	181	ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGGTGGGCTTGGTGGGCCAATCGCTGGTC	240	
Db	181	ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGGTGGGCTTGGTGGGCCAATCGCTGGTC	240	
Qy	241	ATGTTGTGTGATCATCCGATACACAAAGATGAAGACAGCAACCAATTTACATATTTAAC	300	
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Qy	301	CTGGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCCCTTTTCAGAGTAGCGGTCTACTTG	360	
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Qy	361	ATGAATTCCTGGCCTTTTGGGATGTGCTGTGCAAGATAGTAAATTTCCATTGATTACTAC	420	
Db	361	ATGAATTCCTGGCCTTTTGGGATGTGCTGTGCAAGATAGTAAATTTCCATTGATTACTAC	420	
Qy	421	AACATGTTACAGCATCTTCACCTTGAACATGATGAGCGTGGAACCGCTACATTGCCGTG	480	
Db	421	AACATGTTACAGCATCTTCACCTTGAACATGATGAGCGTGGAACCGCTACATTGCCGTG	480	
Qy	481	TGGCACCCCGTGAAGGCTTTGGACTTCCGCACACCCCTTGAAGGCAAGATCATCAATATC	540	
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Qy	541	TGCATTTGGCTGCTGTCATCTGTGTGGCATCTCTGCAATAGTCTTCGGAGCACCAAA	600	
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Qy	601	GTGAGGAGACGTGCATGTGTCATTGAGTCTCTTCGAGTTCACGATGATGACTACTCC	660	
Db	601	GTGAGGAGACGTGCATGTGTCATTGAGTCTCTTCGAGTTCACGATGATGACTACTCC	660	
Qy	661	TGTTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGGCTTCGTGATCCCTGTGCTC	720	
Db	661	TGTTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGGCTTCGTGATCCCTGTGCTC	720	
Qy	721	ATCATCATGCTGTGCTACACCTGATGATCTTCGGTCTCAAGAGCGTCCGGTCTCTTTCT	780	
Db	721	ATCATCATGCTGTGCTACACCTGATGATCTTCGGTCTCAAGAGCGTCCGGTCTCTTTCT	780	

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QY 961 ACCAAGTAGCCTGAATCCCATCTCTAGCCCTTTCTTGATGAAATCTCAAGCGGTGT 1020  
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DB 1141 TGA 1143

RESULT 9  
LOCUS A48343 1142 bp DNA linear PAT 07-MAR-1997  
DEFINITION Sequence 1 from Patent WO9601898.  
ACCESSION A48343  
VERSION A48343.1 GI:2302133  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 1142)  
AUTHORS Kieffer,B. and Simonin,F.  
TITLE HUMAN KAPPA OPIOID RECEPTOR, NUCLEIC ACIDS AND USES THEREOF  
JOURNAL Patent: WO 9601898-A 1 25-JAN-1996;  
UNIV PASTEUR (FR)  
COMMENT Other publication FR 2722209 960112.  
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YSWMDLFMKICVFIFAPVPLIIVCYTLMILRLKSVLLGSREKRLRRLRLV  
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ORIGIN  
Query Match 98.8%; Score 1140.4; DB 6; Length 1142;  
Best Local Similarity 99.9%; Pred. No. 1.6e-199;  
Matches 1141; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 ATGAGTCTCCCGATCCAGATCTTCCGCGGAGCGCGGCCCTTACCTGCGCCCGAGCGCC 60  
DB 1 ATGAGTCTCCCGATCCAGATCTTCCGCGGAGCGCGGCCCTTACCTGCGCCCGAGCGCC 60  
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LOCUS AR141371 1142 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 1 from patent US 6146835.
ACCESSION AR141371
VERSION AR141371.1 GI:15100887
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1142)
AUTHORS Kieffer, B. and Simonin, F.
TITLE Human kappa opioid receptor, nucleic acids and uses thereof
JOURNAL Patent: US 6146835-A 1 14-NOV-2000;
FEATURES
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Location/Qualifiers
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Query Match 98.8%; Score 1140.4; DB 6; Length 1142;
Best Local Similarity 99.9%; Pred. No. 1.6e-199;
Matches 1141; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ATGACTCCCCGATCCAGATCTTCGCGGGGAGCGGCCCTACTCTGGCCCCCGAGCGCC 60
Db 1 ATGACTCCCCGATCCAGATCTTCGCGGGGAGCGGCCCTACTCTGGCCCCCGAGCGCC 60
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LOCUS Homo sapiens opioid receptor kappa (OPR1) mRNA, complete cds.
DEFINITION Homo sapiens opioid receptor kappa (OPR1) mRNA, complete cds.
ACCESSION AF498922
VERSION AF498922.1 GI:20379019
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1143)
AUTHORS Puhl, H.L., Ikeda, S.R. and Aronstam, R.S.
TITLE Direct Submission
JOURNAL Submitted (05-APR-2002) cDNA Resource Center, Guthrie Research Institute, One Guthrie Square, Sayre, PA 18840, USA
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ORIGIN

Query Match 98.6%; Score 1138.2; DB 9; Length 1143;  
Best Local Similarity 99.7%; Pred. No. 4e-199; 3; Indels 0; Gaps 0;  
Matches 1140; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 61 TGCCTGCCCGCCCAACAGCAGCGCTGGTTCCGGCTGGGCCGAGCCCGACAGCAACGGC 120  
DB 61 TGCCTGCCCGCCCAACAGCAGCGCTGGTTCCGGCTGGGCCGAGCCCGACAGCAACGGC 120

QY 121 AGCGCGGCTCGAGGAGCGGAGCTGGAGCGCGCCGACATCTCCCGCGCCATCCCGGTC 180  
DB 121 AGCGCGGCTCGAGGAGCGGAGCTGGAGCGCGCCGACATCTCCCGCGCCATCCCGGTC 180

QY 181 ATCATCACGCGGCTCTACTCCGTTAGTGTTCGTGCTGGGCTTGGTGGGCAACTCGCTGTC 240  
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QY 301 CTGGCTTTGGCAGATGCTTTAGTTACTACAAACATGCCCTTTTCAGAGTACGGTCTACTTG 360  
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QY 541 TGCATCTGGCTGTCTGTCATCTGTGGCATCTCTGCAATAGTCTTGGAGSCACCAA 600  
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QY 601 GTCAGGGAAGACGTGATGTCATGTCATGTCCTTGGAGTTCCTCCAGATGATGACTCTC 660  
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QY 1141 TGA 1143  
DB 1141 TGA 1143

RESULT 12  
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LOCUS AR281680  
DEFINITION Sequence 3 from patent US 6518480.  
ACCESSION AR281680  
VERSION AR281680.1 GI:29717435  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1284)  
AUTHORS Conklin,B.R.  
TITLE Selective target cell activation by expression of a G  
protein-coupled receptor activated superiorly by synthetic ligand  
JOURNAL Patent: US 6518480-A 3 11-FEB-2003;  
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source location/Qualifiers  
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QY 62 GCTGCCCCCAACAGCAGCGCTGTTTCCGCTGGGCCGAGCCCGACAGCAACGGCA 121  
DB 173 GCTGCCCCCAACAGCAGCGCTGTTTCCGCTGGGCCGAGCCCGACAGCAACGGCA 232

QY 122 GCGCGGCTCGAGGAGCGGAGCTGGAGCCCGGACATCTCCCGGCCATCCCGGTCA 181  
DB 233 GCGCGGCTCGAGGAGCGGAGCTGGAGCCCGGACATCTCCCGGCCATCCCGGTCA 292

QY 182 TCATCACGCGGCTCTACTCCGTAGTGTTCGTGGGCTTGGTGGGCAACTCGCTGGTCA 241  
DB 293 TCATCACGCGGCTCTACTCCGTAGTGTTCGTGGGCTTGGTGGGCAACTCGCTGGTCA 352

QY 242 TGTTCGTGATCATCCGATACAAAGATGAAGACAGCAACCAATTTACATTTAAAC 301  
DB 353 TGTTCGTGATCATCCGATACAAAGATGAAGACAGCAACCAATTTACATTTAAAC 412

QY 302 TGGCTTTGGCAGATGCTTTAGTTACTACAAACATGCCCTTTTCAGAGTACGGTCTACTGA 361  
DB 413 TGGCTTTGGCAGATGCTTTAGTTACTACAAACATGCCCTTTTCAGAGTACGGTCTACTGA 472

QY 362 TGAATTTCTGGGCTTTTGGGGATGTCTGTGCAAGATAGTAATTTCCATTTGATTACTA 421  
DB 473 TGAATTTCTGGGCTTTTGGGGATGTCTGTGCAAGATAGTAATTTCCATTTGATTACTA 532

QY 422 ACATGTTTCAACAGATCTTTCACTTGAACATGATGAGCGTGGACCGCTACATTCGCGTGT 481  
DB 533 ACATGTTTCAACAGATCTTTCACTTGAACATGATGAGCGTGGACCGCTACATTCGCGTGT 592

QY 482 GCCACCCCGTGAAGGCTTTGGACTTCCGACACCTTTGAAGGCAAGATCATCAATATCT 541  
DB 541 GCCACCCCGTGAAGGCTTTGGACTTCCGACACCTTTGAAGGCAAGATCATCAATATCT 541

593	GCACCCCGTGAAGCGCTTTGGACATTCCTCGCACACCCCTTGAAGGCAAGAGATCATCAATATCT	652	Matches 1135; Conservative 0; Mismatches 8; Indels 0; Gaps 0
542	GCATCTGGCTGCTGCTGCTATCTCTGTTGGCATCTCTGCAATAGTCTCTTGGAGGACCAAAAG	601	Qy 1 ATGGACTCCCGCATCCAGATCTTCGCGGGAGCGCGGCCCTACCTCGCGCCCGAGCGGC 60
653	GCATCTGGCTGCTGCTGCTATCTCTGTTGGCATCTCTGCAATAGTCTCTTGGAGGACCAAAAG	712	Db 1 ATGGATCCCGCATTCAGATCTTCGCGGGAGCGCTGGGCCCTACCTGCGCCCGAGCGGC 60
602	TCAGGGAAGAGCTGATGTCATTTGAGTGTCTCTTGGATGTCCTCCAGATGATGATCTCTCT	661	Qy 61 TGCCTGCCCCCAACAGCAGCGCTGGTTTCCCGGCTGGGCGAGCCGACAGCAACAGCGC 120
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662	GGTGGGACCTCTTCAATGAAGATCTGCGTCTTCACTTTTGGCTTGGTATCCCTGTCCTCA	721	Qy 121 AGCGCGGCTCGGAGGACCGGAGCTGGAGCCGCGGCACATCTCCCGGCGCATCCCGGTC 180
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LOCUS	Sequence 542 from Patent WO0177172.		
DEFINITION	AX280919		
ACCESSION	AX280919.1	GI:16608215	
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SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
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	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1		
AUTHORS	Lehmann-Bruinsma, K., Liaw, C.W. and Lin, I.L.		
TITLE	Patent: WO 0177172-A 542 18-OCT-2001;		
JOURNAL	Lehmann-Bruinsma, K., Liaw, C.W. and Lin, I.L.		
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QY 1141 TGA 1143  
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Db 1141 TGA 1143

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LOCUS  
DEFINITION Homo sapiens DRG kappa 1 splice variant KOR 1A mRNA, complete cds,  
alternatively spliced.  
ACCESSION AY168006  
VERSION AY168006.1 GI:27373027  
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SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1396)  
Lu, L.D. and Mansson, E.  
Direct Submission  
Submitted (23-OCT-2002) Molecular Biology, Adolor Corporation, 371  
Phoenixville Pike, Malvern, PA 19355, USA  
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ORIGIN  
Query Match 91.6%; Score 1056.8; DB 9; Length 1396;  
Best Local Similarity 96.2%; Pred. No. 3.7e-184;  
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RESULT 15  
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LOCUS  
DEFINITION Sequence 5 from patent US 6518480.  
ACCESSION AR281681  
VERSION AR281681.1 GI:29717436  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1275)  
AUTHORS Conklin, B.R.  
TITLE Selective target cell activation by expression of a G  
protein-coupled receptor activated superiorly by synthetic ligand



JOURNAL Patent: US 6518480-A 5 11-FEB-2003;

FEATURES

Location/Qualifiers

source

1. .1275

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Query Match 86.6%; Score 999.4; DB 6; Length 1275;

Best Local Similarity 93.0%; Pred. No. 1.3e-173;

Matches 1061; Conservative 0; Mismatches 71; Indels 9; Gaps 1;

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Qy 782 GCTCCGAGAGAAAGATCGCAACCTGGTAGGATCACCAGATGCTGCTGGTGGTGGTGG 841
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Qy 842 CAGTCTTCGTGCTGTGCTGGAATCCCATTTACATATTTACATCTCTGTTGGAGGCTCTGGGA 901
Db 944 CAGTCTTCGTGCTGTGCTGGAATCCCATTTACATATTTACATCTCTGTTGGAGGCTCTGGGA 1003
Qy 902 GCACCTCCCAACAGCAGCTGCTCTCTCCAGCTATTAATTTCTGCAATGCTTAGGCTATA 961
Db 1003 GCACCTCCCAACAGCAGCTGCTCTCTCCAGCTATTAATTTCTGCAATGCTTAGGCTATA 1063
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Qy 962 CCAACAGTAGCTGAATCCCATTTCTTACGCTTTCTTGTATGAAATCTTCAAGCGGTGTT 1021
Db 1064 CCAACAGTAGCTGAATCCCATTTCTTACGCTTTCTTGTATGAAATCTTCAAGCGGTGTT 1123
Qy 1022 TCCGGGACTTCTGCTTTTCCACTGAAGATGAGGATGGAGCGGACAGCACTAGCAGAGTCC 1081
Db 1124 TCCGGGACTTCTGCTTTTCCACTGAAGATGAGGATGGAGCGGACAGCACTAGCAGAGTCC 1183
Qy 1082 GAAATACAGTTTCAGGATCTGCTTACCTGAGGGACATCGATGGGATGAATAAACAGTAT 1141
Db 1184 GAAATACAGTTTCAGGATCTGCTTACCTGAGGGACATCGATGGGATGAATAAACAGTAT 1243
Qy 1142 G 1142
Db 1244 G 1244
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Job time : 5377.67 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 6, 2005, 12:28:42 ; Search time 700.667 Seconds  
(without alignments)  
9749.831 Million cell updates/sec

Title: US-09-904-584-3  
Perfect score: 1154  
Sequence: 1 atgagatccccgcatccagat.....ccagatgactagctgga 1154

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*

- 1: Geneseqn1980s:\*
- 2: Geneseqn1990s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002as:\*
- 7: Geneseqn2002bs:\*
- 8: Geneseqn2003as:\*
- 9: Geneseqn2003bs:\*
- 10: Geneseqn2003cs:\*
- 11: Geneseqn2003ds:\*
- 12: Geneseqn2004as:\*
- 13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1154	100.0	1154	12	ADN30507 Human kap
2	1152.4	99.9	1154	12	ADN30505 Human kap
3	1152.4	99.9	1154	13	ADR44858 Human kap
4	1150.8	99.7	1154	12	ADN30506 Human kap
5	1150.8	99.7	1154	12	ADN30510 Human kap
6	1150.8	99.7	1154	12	ADN30508 Human kap
7	1150.8	99.7	1154	12	ADN30511 Human kap
8	1150.8	99.7	1154	12	ADN30509 Human kap
9	1144.4	99.2	1182	8	ABZ42678 Human opi
10	1144.4	99.2	1182	10	AAD58490 Human kap
11	1144.4	99.2	1182	10	ADZ4861 Farnesyl
12	1144.4	99.2	1182	10	ACA56819 Human sig
13	1144.4	99.2	1182	12	ADI56615 Human pol
14	1141.4	98.9	1143	2	AAT90998 Human kap
15	1140.4	98.8	1142	2	AAT12550 Human kap
16	1136.2	98.5	1284	2	AAT90999 Human kap
17	1136.2	98.5	1284	11	ADL90106 Human kap
18	1133.4	98.2	1143	12	ADO30011 Human GPC
19	1130.2	97.9	1143	5	ABI98011 Non-endog
20	999.4	86.6	1275	2	AAT92601 Human kap

21	999.4	86.6	1275	11	ADL90108 Human kap
22	994.6	86.2	1275	11	ADL90110 Human kap
23	979.4	84.9	1875	11	ADL90116 Human kap
24	963.4	83.5	1875	11	ADL90118 Human kap
25	912.4	79.1	1408	2	AAV49254 Mouse kap
26	912.4	79.1	1410	2	AAQ75926 Mouse kap
27	912.4	79.1	1410	13	ADR44860 Mouse kap
28	912.4	79.1	2481	2	AAQ86725 Mammalian
29	912.4	79.1	2481	13	ADR44862 Rat kappa
30	901.4	78.1	1143	12	ADO30301 Mouse GPC
31	877.8	76.1	1911	11	ADL90120 Human kap
32	868	75.2	1000	2	AAQ75931 Human kap
33	449.6	39.0	2135	5	AAF85416 Nucleotid
34	448	38.8	1401	13	ADR44848 Rat mu op
35	448	38.8	1618	2	AAQ89222 Rat mu op
36	448	38.8	1618	2	AAQ89223 Transcrip
37	448	38.8	1618	3	AA559499 cDNA enco
38	445	38.6	2070	2	AAQ79199 Rat mu-su
39	440	38.1	9426	13	ADR44835 FIV opioi
40	440	38.1	9569	13	ADR44842 FIV-NSE-H
41	440	38.1	10472	13	ADR44876 Plasmid p
42	438	38.0	2162	2	AAV61994 Human mu-
43	437.8	37.9	1464	10	ADG42250 Mu-opioid
44	436.4	37.8	1200	13	ADR44830 Human HUM
45	436.4	37.8	1200	13	ADR44837 HUMOR mut

ALIGNMENTS

RESULT 1  
ADN30507  
ID ADN30507 standard; cDNA; 1154 BP.

AC ADN30507;

DT 12-AUG-2004 (first entry)

DE Human kappa opioid receptor, hKOR, C948T allele.

XX Human; kappa opioid receptor; hKOR; ss; gene; SNP;  
KW single nucleotide polymorphism; endogenous opioid system; nociception;  
KW neurotransmitter release; learning; memory; cognition; pain; cocaine;  
KW amphetamine; alcohol; tobacco; opiate; withdrawal;  
KW neuroendocrine function; reproductive function; prolactin regulation;  
KW stress responsiveness; mood; affect; immune function;  
KW gastrointestinal function; analgesia; addictive disease;  
KW chromosome 8q11.2.

OS Homo sapiens.

PH Key Location/Qualifiers  
FT allele replace(948,C)  
FT /\*tag= a

US2004097704-A1

PD 20-MAY-2004.

XX 13-JUL-2001; 2001US-00904584.

XX 14-JUL-2000; 2000US-0218300P.

XX (KREE/) KREEK M J.

PA (YUFE/) YUFEROV V.

PA (LAFO/) LAFORGE K S.

PI Kreek MJ, Yufarov V, Laforge KS;

XX WPI; 2004-389204/36.

XX Novel isolated variant allele of human kappa opioid receptor gene, useful



variation	/standard_name="Single nucleotide polymorphism" replace(843,G) /*tag= b
variation	/standard_name="Single nucleotide polymorphism" replace(846,T) /*tag= c
variation	/standard_name="Single nucleotide polymorphism" replace(852,T) /*tag= d
variation	/standard_name="Single nucleotide polymorphism" replace(948,T) /*tag= e
variation	/standard_name="Single nucleotide polymorphism" replace(1008,T) /*tag= f

US2004097704-A1.

20-MAY-2004.

13-JUL-2001; 2001US-00904584.

14-JUL-2000; 2000US-0218300P.

(KREE/) KREEK M J.  
(YUFE/) YUFEROV V.  
(LAFO/) LAFORGE K S

Kreek MJ, Yuferov V, Laforge KS;

WPI; 2004-389204/36.

Novel isolated variant allele of human kappa opioid receptor gene, useful for determining susceptibility in subject to physiological response, condition or disease related to endogenous opioid system.

Claim 1; SEQ ID NO 1; 29pp; English.

The invention relates to an isolated variant allele of a human kappa opioid receptor gene, comprising a DNA sequence having at least one variation in a fully defined wild-type allele of human kappa opioid receptor (hKOR) sequence appearing as ADN30505, where the variation comprises C852T, C948T, C1008T or their combinations. Also included are an isolated nucleic acid molecule selectively hybridising to the variant, a cloning vector comprising the variant and an origin of replication, an expression vector comprising the variant associated with a promoter, a unicellular host transformed/transfected with the vector and a commercial test kit for determining the presence of at least one variation in a hKOR gene of an allele in a bodily sample taken from a subject. The hKOR variant allele is useful for determining a susceptibility in a subject to at least one physiological response, condition or disease related to the endogenous opioid system, nociception, neurotransmitter release endogenous opioid system, learning, memory, cognition, pain, cocaine, amphetamine and other stimulants self-administration, behavioural sensitisation to cocaine, opiates, alcohol and tobacco, opiate, amphetamine and alcohol withdrawal, physical dependence and tolerance; neuroendocrine function, reproductive function, prolactin regulation, stress responsiveness, physiology and pathology of mood and affect, immune function, gastrointestinal function. The hKOR variant allele is useful for determining a susceptibility to pain in a subject and is useful for determining a therapeutically effective amount of pain reliever to administer to a subject in order to induce analgesia in the subject. The hKOR variant allele is useful for determining a therapeutically effective amount of therapeutic agent to administer to a subject suffering from at least one addictive disease to treat the at least one addictive disease. The gene for hKOR is located on chromosome 8q11.2. The present sequence is the most common, wild-type allele of hKOR.

Sequence 1154 BP; 239 A; 339 C; 287 G; 289 T; 0 U; 0 Other;

### Query Match

Query Match	99.9%;	Score 1152.4;	DB 12;	Length 1154;
Best Local Similarity	99.9%;	Pred. No. 6.7e-273;		

	Matches 1153;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;	
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Db	1	ATG	ACTCC	CCCGATCC	CAGATCT	TC	CGCGGGAG	CCGGCCCT	ACTCTCGCCCCGAGCGCC	60
Qy	61	TGC	TGCCCC	CCCAAC	CAGACGGC	TGG	TTTCC	CGGCTT	TGGCCGAGCCCGACGACGCGC	120
Db	61	TGC	TGCCCC	CCCAAC	CAGACGGC	TGG	TTTCC	CGGCTT	TGGCCGAGCCCGACGACGCGC	120
Qy	121	AGG	CCGGCT	CGGAGG	CGCAGCT	TGG	AGCCG	CGCCAC	ATCTCTCCCGGCCATCCCGGTC	180
Db	121	AGG	CCGGCT	CGGAGG	CGCAGCT	TGG	AGCCG	CGCCAC	ATCTCTCCCGGCCATCCCGGTC	180
Qy	181	ATC	ATCAGCG	CGGTCT	ACTCCG	TAGTGT	TTCG	TGCGGGCT	TGTTGGGCAACTCGCTGGTC	240
Db	181	ATC	ATCAGCG	CGGTCT	ACTCCG	TAGTGT	TTCG	TGCGGGCT	TGTTGGGCAACTCGCTGGTC	240
Qy	241	ATG	TTGCGT	GATCAT	CCGATAC	CAAA	GATGA	GACAGCAAC	CAATTTTACATATTTTAAC	300
Db	241	ATG	TTGCGT	GATCAT	CCGATAC	CAAA	GATGA	GACAGCAAC	CAATTTTACATATTTTAAC	300
Qy	301	CTG	CTTTGG	CAGATCT	TTAGTT	TACT	ACAA	CCATGCC	TTTCAGAGTAGCGTCTACTTG	360
Db	301	CTG	CTTTGG	CAGATCT	TTAGTT	TACT	ACAA	CCATGCC	TTTCAGAGTAGCGTCTACTTG	360
Qy	361	ATG	AATTCCT	TGGCCT	TTTGGG	GATGT	CTGT	CAAGAT	AGTAAATTTCCATTGATTACTAC	420
Db	361	ATG	AATTCCT	TGGCCT	TTTGGG	GATGT	CTGT	CAAGAT	AGTAAATTTCCATTGATTACTAC	420
Qy	421	AAC	ATGTTT	CACAGCA	TCTT	CACCT	TGAC	ATGAT	GAGCGTGGACCGCTACATTTGCCGTG	480
Db	421	AAC	ATGTTT	CACAGCA	TCTT	CACCT	TGAC	ATGAT	GAGCGTGGACCGCTACATTTGCCGTG	480
Qy	481	TGC	ACCCCG	TGAAGC	TTTGG	ATCT	TCGCA	CACCTT	GAAAGCAAGATCATCAATATC	540
Db	481	TGC	ACCCCG	TGAAGC	TTTGG	ATCT	TCGCA	CACCTT	GAAAGCAAGATCATCAATATC	540
Qy	541	TGC	ATCTGG	CTGCTGT	CTCAT	CTGT	TGGCAT	CTCTG	CAATAGTCTCTGGAGGCACCAA	600
Db	541	TGC	ATCTGG	CTGCTGT	CTCAT	CTGT	TGGCAT	CTCTG	CAATAGTCTCTGGAGGCACCAA	600
Qy	601	GT	CAGGAA	AGACGT	CGATGT	CAIT	TGAGT	GCTCCT	TGCAGTCCCAGATGATGACTCTCC	660
Db	601	GT	CAGGAA	AGACGT	CGATGT	CAIT	TGAGT	GCTCCT	TGCAGTCCCAGATGATGACTCTCC	660
Qy	661	TGT	TGGAC	CTTCT	CATGA	AGATCT	CGGT	CTTCAT	CTTTGCCCTTGTGATCCCTGTCTC	720
Db	661	TGT	TGGAC	CTTCT	CATGA	AGATCT	CGGT	CTTCAT	CTTTGCCCTTGTGATCCCTGTCTC	720
Qy	721	ATC	ATCAT	CGTCTG	CTAC	CCCTG	ATGAT	CTCTG	CGTCTCAAGAGCGTCCGGCTCTTCT	780
Db	721	ATC	ATCAT	CGTCTG	CTAC	CCCTG	ATGAT	CTCTG	CGTCTCAAGAGCGTCCGGCTCTTCT	780
Qy	781	GGC	TCCCG	AGAGAA	AGATCG	CAAC	CTCGT	TAGSAT	CACCAGACTTGTCTCTGTGTGGTGTG	840
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Qy	841	GCA	GCTCT	CGTCTG	CTGTG	BACT	CCCAT	TCATAT	TTCCTGTGTGAGGCTCTGGGG	900
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Qy	901	AGC	ACCTCC	CAAG	CACAG	CTG	CTCTC	CAAGTAT	TACTCTGCAATTCGCTTAGGCTAT	960
Db	901	AGC	ACCTCC	CAAG	CACAG	CTG	CTCTC	CAAGTAT	TACTCTGCAATTCGCTTAGGCTAT	960
Qy	961	ACCA	ACAGT	AGCTGA	ATCC	CAATCT	CTAC	GGCTTT	CTTGTGATGAATCTCAAGCGGTCT	1020
Db	961	ACCA	ACAGT	AGCTGA	ATCC	CAATCT	CTAC	GGCTTT	CTTGTGATGAATCTTCAAGCGGTCT	1020
Qy	1021	TT	CCGGGA	TTTCTG	CTTTT	CCACT	GAAGAT	GAGGAT	TGGAGCGCAGACGACTAGCAGATC	1080
Db	1021	TT	CCGGGA	TTTCTG	CTTTT	CCACT	GAAGAT	GAGGAT	TGGAGCGCAGACGACTAGCAGATC	1080

QY 1081 CGAAATACAGTTCCAGGATCTGTTACCTGAGGACATCGATGGGATGAATAAACAGTA 1140  
 DB 1081 CGAAATACAGTTCCAGGATCTGTTACCTGAGGACATCGATGGGATGAATAAACAGTA 1140  
 QY 1141 TGAAGTCTGCTGGA 1154  
 DB 1141 TGAAGTCTGCTGGA 1154

RESULT 3  
 ADR44858  
 ID ADR44858 standard; cDNA; 1154 BP.  
 XX  
 AC ADR44858;  
 DT 18-NOV-2004 (first entry)  
 XX  
 DE Human kappa opioid receptor encoding cDNA SEQ ID NO:30.  
 XX  
 KW opioid receptor; nerve cell; analgesic; gene therapy; pain; human;  
 KW kappa opioid receptor; chromosome 8; gene; ss.  
 XX  
 OS Homo sapiens.

PH Key Location/Qualifiers  
 FT CDS 1..1143  
 FT /\*tag= a  
 FT /product= "kappa opioid receptor"

XX WO2004073646-A2.  
 XX  
 XX 02-SEP-2004.  
 XX  
 XX 19-FEB-2004; 2004WO-US004914.  
 XX  
 XX 19-FEB-2003; 2003US-0448663P.  
 XX  
 XX (UYRP ) UNIV ROCHESTER.  
 XX  
 XX Kyrkanides S, Tallents RH;  
 XX  
 XX WPI; 2004-635472/61.  
 DR P-PSDB; ADR44857.  
 DR GENBANK; U17298.

XX New vector for delivering an opioid receptor to a nerve cell comprising a  
 PT sequence encoding a mu-opioid receptor and a vector backbone, useful in  
 PT preparing a composition for reducing pain.

XX Disclosure; SEQ ID NO 30; 147bp; English.  
 XX  
 CC The present invention describes a vector for delivering an opioid  
 CC receptor to a nerve cell. The method comprises a sequence encoding an  
 CC opioid receptor and a vector backbone. Also described: (1) a cell  
 CC comprising the vector or its integrated product; (2) an animal comprising  
 CC the cell; (3) reducing pain in a subject; (4) producing the vector; (5)  
 CC producing the cell; and (6) an animal produced by the process of  
 CC administering the vector to the animal. The vector has analgesic  
 CC activity, and can be used in gene therapy. The vector is useful in  
 CC preparing a composition for reducing pain in a subject. The present  
 CC sequence encodes the human kappa opioid receptor, which is used in the  
 CC exemplification of the present invention. The human kappa opioid receptor  
 CC gene is located on chromosome 8, more specifically to 8q11-12.  
 XX  
 XX Sequence 1154 BP; 239 A; 339 C; 287 G; 289 T; 0 U; 0 Other;

Query Match 99.9%; Score 1152.4; DB 13; Length 1154;  
 Best Local Similarity 99.9%; Pred. No. 6.7e-273;  
 Matches 1153; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 ATGAGTCTCCCGATCCAGATCTTCCGCGGGAGCCGGGCTTACCTGCGCCCGAGCGCC 60  
 QY 61 TGCCTGCCCGCCCAACAGCAGCGGCTGTTTCCCGGCTGGCGGAGCCCGACAGCAACGCGC 120  
 DB 61 TGCCTGCCCGCCCAACAGCAGCGGCTGTTTCCCGGCTGGCGGAGCCCGACAGCAACGCGC 120  
 QY 121 AGCGCCGGCTCGGAGGAGCGCAGCTGGAGCGCGGCACATCTCCCGCGCCATCCCGGTC 180  
 DB 121 AGCGCCGGCTCGGAGGAGCGCAGCTGGAGCGCGGCACATCTCCCGCGCCATCCCGGTC 180  
 QY 181 ATCATCAGCGGCTTACTCCGTAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
 DB 181 ATCATCAGCGGCTTACTCCGTAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
 QY 241 ATGTTCTGTGATCATCCGATACACAAAGATGAAGACAGCAACCAATTTTACATTTTAA 300  
 DB 241 ATGTTCTGTGATCATCCGATACACAAAGATGAAGACAGCAACCAATTTTACATTTTAA 300  
 QY 301 CTGGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCCCTTTTCAGAGTACGGTCTACT 360  
 DB 301 CTGGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCCCTTTTCAGAGTACGGTCTACT 360  
 QY 361 ATGAATTCCTGGCTTTTGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
 DB 361 ATGAATTCCTGGCTTTTGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
 QY 421 AACATGTTTACCAGCATCTTACCTTGACATGATGAGCGTGACCGCTACATTTGCCGTG 480  
 DB 421 AACATGTTTACCAGCATCTTACCTTGACATGATGAGCGTGACCGCTACATTTGCCGTG 480  
 QY 481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCAACACCTTTGAAGGCAAGATCATCAATATC 540  
 DB 481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCAACACCTTTGAAGGCAAGATCATCAATATC 540  
 QY 541 TGCATCTGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
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 DB 601 GTGAGGAGAGCTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
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 QY 721 ATCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
 DB 721 ATCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
 QY 781 GGCTCCCGAGAGAAAGATCGCAACCTGCTAGGATCACCAGACTGGTCTGCTGCTGCTGCTG 840  
 DB 781 GGCTCCCGAGAGAAAGATCGCAACCTGCTAGGATCACCAGACTGGTCTGCTGCTGCTGCTG 840  
 QY 841 GCAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
 DB 841 GCAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
 QY 901 AGACCTCCACAGCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
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QY 1141 TGACTAGTCGTGGA 1154  
 Db |||||

RESULT 4  
 ADN30506  
 ID ADN30506 standard; cDNA; 1154 BP.  
 XX  
 AC ADN30506;  
 XX  
 DT 12-AUG-2004 (first entry)  
 XX  
 DE Human kappa opioid receptor, hKOR, C852T allele.  
 XX  
 KW Human; kappa opioid receptor; hKOR; ss; gene; SNP;  
 KW single nucleotide polymorphism; endogenous opioid system; nociception;  
 KW neurotransmitter release; learning; memory; cognition; pain; cocaine;  
 KW amphetamine; alcohol; tobacco; opiate; withdrawal;  
 KW neuroendocrine function; reproductive function; prolactin regulation;  
 KW stress responsivity; mood; affect; immune function;  
 KW gastrointestinal function; analgesia; addictive disease;  
 KW chromosome 8q11.2.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT allele replace(852,C)  
 FT /\*tag= a  
 FT /standard\_name= "single nucleotide polymorphism"  
 XX  
 PN US2004097704-A1.  
 XX  
 PD 20-MAY-2004.  
 XX  
 PF 13-JUL-2001; 2001US-00904584.  
 XX  
 PR 14-JUL-2000; 2000US-0218300P.  
 XX  
 PA (KREE/) KREEK M J.  
 PA (YUPE/) YUFEROV V.  
 PA (LAFO/) LAFORGE K S.  
 XX  
 PI Kreek MJ, Yufarov V, Laforge KS;  
 XX  
 DR WPI; 2004-389204/36.  
 XX  
 PT Novel isolated variant allele of human kappa opioid receptor gene, useful  
 PT for determining susceptibility in subject to physiological response,  
 PT condition or disease related to endogenous opioid system.  
 XX  
 PS Example; SEQ ID NO 2; 29pp; English.  
 XX

CC stress responsivity, physiology and pathology of mood and affect, immune  
 CC function, gastrointestinal function. The hKOR variant allele is useful  
 CC for determining a susceptibility to pain in a subject and is useful for  
 CC determining a therapeutically effective amount of pain reliever to  
 CC administer to a subject in order to induce analgesia in the subject. The  
 CC hKOR variant allele is useful for determining a therapeutically effective  
 CC amount of therapeutic agent to administer to a subject suffering from at  
 CC least one addictive disease to treat the at least one addictive disease.  
 CC The gene for hKOR is located on chromosome 8q11.2. The present sequence  
 CC is the C852T allele of hKOR.  
 XX  
 SQ Sequence 1154 BP; 239 A; 338 C; 287 G; 290 T; 0 U; 0 Other;  
 XX

Query Match 99.7%; Score 1150.8; DB 12; Length 1154;  
 Best Local Similarity 99.8%; Pred. No. 1.7e-272;  
 Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGACTCCCGATCCAGATCTTCGGGGGAGCGGGCCCTACTGCGCCCGAGCGCC 60  
 Db |||||

Db 1 ATGACTCCCGATCCAGATCTTCGGGGGAGCGGGCCCTACTGCGCCCGAGCGCC 60  
 |||||

Qy 61 TGCCTGCCCGCCCAACAGCGCGCTGGTTCCCGGCTGGGCGGAGCGCCGAGCAACGGC 120  
 Db |||||

Db 61 TGCCTGCCCGCCCAACAGCGCGCTGGTTCCCGGCTGGGCGGAGCGCCGAGCAACGGC 120  
 |||||

Qy 121 AGCGCCGGCTCGGAGGACGGCGAGCTGGAGCGCCCGCACATCTCCCGGGCCATCCCGGTC 180  
 Db |||||

Db 121 AGCGCCGGCTCGGAGGACGGCGAGCTGGAGCGCCCGCACATCTCCCGGGCCATCCCGGTC 180  
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Qy 181 ATCATACGGCGGTCTACTCCGTAGTGTTCGTCTGGGCTGGGCGAACTCGCTGTC 240  
 Db |||||

Db 181 ATCATACGGCGGTCTACTCCGTAGTGTTCGTCTGGGCTGGGCGAACTCGCTGTC 240  
 |||||

Qy 241 ATGTTCTGTATCATCCGATACACAAAGATGAAGACAGCAACCAATTTACATTTTAAAC 300  
 Db |||||

Db 241 ATGTTCTGTATCATCCGATACACAAAGATGAAGACAGCAACCAATTTACATTTTAAAC 300  
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Qy 301 CTGGCTTTGGCAGATGCTTTTAGTTACTACAAACCATGCTTTTCAGAGTACCGTCTACTTG 360  
 Db |||||

Db 301 CTGGCTTTGGCAGATGCTTTTAGTTACTACAAACCATGCTTTTCAGAGTACCGTCTACTTG 360  
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Qy 361 ATGAATTCCTGGCCCTTTTGGGGATGTGTGTGCAAGATAGTAATTCATTTGATATAC 420  
 Db |||||

Db 361 ATGAATTCCTGGCCCTTTTGGGGATGTGTGTGCAAGATAGTAATTCATTTGATATAC 420  
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Qy 421 AACATGTTCCAGCATCTTCACCTTCACCATGATGAGCGTGGACCGCTACATTTGCCGTG 480  
 Db |||||

Db 421 AACATGTTCCAGCATCTTCACCTTCACCATGATGAGCGTGGACCGCTACATTTGCCGTG 480  
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Qy 481 TGCACCCCGTGAAGGCTTTGGACTTCGGACATGAGCGTGGACCGCTACATTTGCCGTG 540  
 Db |||||

Db 481 TGCACCCCGTGAAGGCTTTGGACTTCGGACATGAGCGTGGACCGCTACATTTGCCGTG 540  
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Qy 541 TGCATCTGGT 600  
 Db |||||

Db 541 TGCATCTGGT 600  
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Qy 601 GTGAGGAAGACGTCGATGTCATTGAGTGTCTTGGAGTTCAGTTCAGATGATGATCTCC 660  
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Db 601 GTGAGGAAGACGTCGATGTCATTGAGTGTCTTGGAGTTCAGTTCAGATGATGATCTCC 660  
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Qy 661 TGGTGGGACCTCTTTCATGAAGATCTGGCTTTCATCTTTTGGCTTCGTGTCTCTCTCT 720  
 Db |||||

Db 661 TGGTGGGACCTCTTTCATGAAGATCTGGCTTTCATCTTTTGGCTTCGTGTCTCTCTCT 720  
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Qy 721 ATCATATCTGT 780  
 Db |||||

Db 721 ATCATATCTGT 780  
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Qy 781 GGCTCCCGAGGAAGATCCCAACCTCGGTAGGATCACCAGACTGGTCTGGTGGTGGTGG 840  
 Db |||||

Db 781 GGCTCCCGAGGAAGATCCCAACCTCGGTAGGATCACCAGACTGGTCTGGTGGTGGTGG 840  
 |||||



Qy	841	GCAGTCTTCGTCGTCGTCGAGATCCCAATTCACATATTCTCTGCTGGAGGCTCTGGGG	900
Db	841	GCAGTCTTCGTCGTCGTCGAGATCCCAATTCACATATTCTCTGCTGGAGGCTCTGGGG	900
Qy	901	AGCACCTCCACAGCACAGCTGCTCTCTCAGGCTATTACTTTCGATTTGCTTAGGCTAT	960
Db	901	AGCACCTCCACAGCACAGCTGCTCTCTCAGGCTATTACTTTCGATTCGCTTAGGCTAT	960
Qy	961	ACCAACGATGAGCTGAATCCGATTCCTCTAGCCCTTTCTTGATGAAACACTTCAAGCGGTG	1020
Db	961	ACCAACGATGAGCTGAATCCGATTCCTCTAGCCCTTTCTTGATGAAACACTTCAAGCGGTG	1020
Qy	1021	TTCCGGGACATTCGCTTTTCCACTGAAGATGAGGCGGACAGACACTAGCAGAGTC	1080
Db	1021	TTCCGGGACATTCGCTTTTCCACTGAAGATGAGGCGGACAGACACTAGCAGAGTC	1080
Qy	1081	CGAATAACAGTTCAGGATCCTGCTTACCTCAGGGACATCGATGGGATGAATAAACAGTA	1140
Db	1081	CGAATAACAGTTCAGGATCCTGCTTACCTCAGGGACATCGATGGGATGAATAAACAGTA	1140
Qy	1141	TGACTAGTCGTGGA	1154
Db	1141	TGACTAGTCGTGGA	1154

## RESULT 5

RESORT 2  
ADN30510

ADN30510  
ID ADN30510 standard: cDNA: 1154 BP.

XX  
ID ADN50510

AC ADN30510:

AC  
XX  
ADN30310;

12-AUG-2004 (first entry)

DT 12-AUG-2004 (LTPC ENCLY)  
XX

XX  
DE Human kappa oncid receptor. hKOR. A843G allele.

DE  
yy  
Human kappa kappa receptor, mouse, mouse antigen.

XX	human	Yanna	oncid	receptor	hKOR	ss	gene	SNP
XX								

Human; kappa opioid receptor; INOR; ss; gene; snf; KW  
single nucleotide polymorphism: endogenous opioid system: nociception

single nucleotide polymorphism; endogenous opioid system; nociception; neurotransmitter release; learning; memory; cognition; pain; cocaine; KW

KW neurotransmitter release; learning; memory; cognition; pain; cocaine;  
WZ amphetamine; alcohol; tobacco; opiate; withdrawal:

amphetamines; alcohol; tobacco; opiates; withdrawal;  
reproductive function: prolactin regulation:

neuroendocrine function; reproductive function; prolactin regulation; immune function; effect; need; effect; immune function;

stress responsivity,; mood; affect; immune function;  
stress responsivity,; mood; affect; immune function;  
stress responsivity,; mood; affect; immune function;

KW gastrointestinal function; analgesia; addictive disease;

KW chromosome 8q11.2.

XXV

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
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100	100	100

FT allele  
replace(843,A)

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ET /*tag= a
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FT /standard\_name= "Single nucleotide polymorphism"

XX

PN US2004097704-A1.

XX

PD 20-MAY-2004.

**XX**

PF 13-JUL-2001; 2001US-00904584.

17 XX

PR 14-JUL-2000; 2000US-0218300P.

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16  
15  
14  
13  
12  
11  
10  
9  
8  
7  
6  
5  
4  
3  
2  
1

PA (KREE/) KREE M J.

PA (KKEE/) KKEER M. S.;  
PA (YUFE/) YUFEROV V.

	Db	 TGCATCTGGCTGCTGTCGTCACTCGTTGGCATCTCTGCAATAGTCCCTTGGAGGCCACCAA	600
	Qy	 GTCAGGGAAGAAGCGTCGATGTCATTGAGTGCTCCTTTGCAGTTGCCAAGATGATGACTACTCC	660
	Db	 GTCAGGGAAGAAGCGTCGATGTCATTGAGTGCTCCTTTGCAGTTGCCAAGATGATGACTACTCC	660
	Qy	 TGGTGGGACCTCTTCATGAAGATCTGCGGCTTCATCTTTGGCTTCGTCGATCCCTGTCCTC	720
	Db	 TGGTGGGACCTCTTCATGAAGATCTGCGGCTTCATCTTTGGCTTCGTCGATCCCTGTCCTC	720
	Qy	 ATCATCATCTGCTCTGCATCACACCTCGATGATCTCTGCGTCTCAAGAGCGTCGGGCTCCTTTCT	780
	Db	 ATCATCATCTGCTCTGCATCACACCTCGATGATCTCTGCGTCTCAAGAGCGTCGGGCTCCTTTCT	780
	Qy	 GGCTCCCGAGAGAAGATCGCAACCTGCGTAGGATCACAGACTGGTCTCTGGTGGTGGTG	840
	Db	 GGCTCCCGAGAGAAGATCGCAACCTGCGTAGGATCACAGACTGGTCTCTGGTGGTGGTG	840
	Qy	 GCAGTCTTTCGTGCTCTGCTGGACTCCCATTACATAATTCATCTCGTGGAGGCTCTGGGG	900
	Db	 GCAGTCTTTCGTGCTCTGCTGGACTCCCATTACATAATTCATCTCGTGGAGGCTCTGGGG	900
	Qy	 AGCACTCCCAACAGACAGCTGCTCTCTCAGCTATTACTTCTGCAATTCGCTTAAGGCTAT	960
	Db	 AGCACTCCCAACAGACAGCTGCTCTCTCAGCTATTACTTCTGCAATTCGCTTAAGGCTAT	960
	Qy	 ACCAACAGTAGCCCTGAATCCCAATTCCTPACGCCCTTTCTTGATGAAACCTCCAAGCGGT	1020
	Db	 ACCAACAGTAGCCCTGAATCCCAATTCCTPACGCCCTTTCTTGATGAAACCTCCAAGCGGT	1020
	Qy	 TTCCGGGACTTCTGCTTTTCCACTGAAGATGAGGATGGAGCGGCAGAGCACTAGCAGATC	1080
	Db	 TTCCGGGACTTCTGCTTTTCCACTGAAGATGAGGATGGAGCGGCAGAGCACTAGCAGATC	1080
	Qy	 CGAAATACAGTTCCAGGATCCTGCTTTACTCGAGGACATCCGATGGATGCAATAAACCAGTA	1140
	Db	 CGAAATACAGTTCCAGGATCCTGCTTTACTCGAGGACATCCGATGGATGCAATAAACCAGTA	1140
	Qy	 TGACTAGTCGTGGA	1154
	Db	 TGACTAGTCGTGGA	1154

RESULT 6  
ADN30508  
ID ADN30508 standard; cDNA; 1154 BP.  
XX  
AC ADN30508;

DT 12-AUG-2004 (first entry)

XX  
DE  
Human kappa opioid receptor, hKOR, C1008T allele.

Human; kappa opioid receptor; hKOR; ss; gene; SNP;  
single nucleotide polymorphism; endogenous opioid system; nociception;  
KW neurotransmitter release; learning; memory; cognition; pain; cocaine;  
KW amphetamine; alcohol; tobacco; opiate; withdrawal;  
KW neuroendocrine function; reproductive function; prolactin regulation;  
KW stress responsiveness; mood; affect; immune function;  
KW gastrointestinal function; analgesia; additive disease;  
KW chromosome 8all.2

OS Homo sapiens.

AA	
FH	Key
FT	allele
FT	Location/Qualifiers replace(1008,C) /*tag= a
FT	/standard name= "Siri"

XX  
PN  
US2004097704-A1.

20-MAY-2004.

[illegible]

13-JUL-2001; 2001US-00904584.

14-JUL-2000; 2000US-0218300P.

(KREE/) KREEK M J.

(LAFE//) LAFORE V.  
(LAFO//) LAFORE K S

Kreek MJ, Yuferov V

WPI: 2004-389204/36.

Novel isolated varia

for determining susceptibility in subject to physiological response, condition or disease related to endogenous opioid system

Example 10. CEO ID NO A. 2000. English

The invention relates to an isolated variant allele of a human kappa opioid receptor gene, comprising a DNA sequence having at least one variation in a fully defined wild-type allele of human kappa opioid receptor (hKOR) sequence appearing as ADN30505, where the variation comprises C852T, C948T, C1008T or their combinations. Also included are an isolated nucleic acid molecule selectively hybridising to the variant, a cloning vector comprising the variant and an origin of replication, an expression vector comprising the variant associated with a promoter, a unicellular host transformed/transfected with the vector and a commercial test kit for determining the presence of at least one variation in a hKOR gene of an allele in a bodily sample taken from a subject. The hKOR variant allele is useful for determining a susceptibility in a subject to at least one physiological response, condition or disease related to the endogenous opioid system, nociception, neurotransmitter release endogenous opioid system, learning, memory, cognition, pain, cocaine, amphetamine and other stimulants self-administration, behavioural sensitisation to cocaine, opiates, alcohol and tobacco, opiate, amphetamine and alcohol withdrawal, physical dependence and tolerance; neuroendocrine function, reproductive function, prolactin regulation, stress responsiveness, physiology and pathology of mood and affect, immune function, gastrointestinal function. The hKOR variant allele is useful for determining a susceptibility to pain in a subject and is useful for determining a therapeutically effective amount of pain reliever to administer to a subject in order to induce analgesia in the subject. The hKOR variant allele is useful for determining a therapeutically effective amount of therapeutic agent to administer to a subject suffering from at least one addictive disease to treat the at least one addictive disease. The gene for hKOR is located on chromosome 8q11.2. The present sequence is the C1008T allele of hKOR.

Sequence 1154 BP; 239 A; 338 C; 287 G; 290 T; 0 U; 0 Other;

Query Match	99.7%	Score 1150.8	DB 12	Length 1154
Best Local Similarity	99.8%	Pred. No. 1.7e-272		
Matches 1152	Conservative 0	Mismatches 2	Indels 0	Gaps 0
Qy	1	ATGAGCTCCCGCATCCAGATCTTCGGCGGGAGCGGGCCCTACTCGCGCCCGAGCGCC	60	
Db	1	ATGAGCTCCCGCATCCAGATCTTCGGCGGGAGCGGGCCCTACTCGCGCCCGAGCGCC	60	
Qy	61	TGGCTGCCCCCAACAGCAGCGCGCTGGTTTCGGGCTGGGCGGAGCCCGACAGCAACCGC	120	
Db	61	TGCTGCCCCCAACAGCAGCGCGCTGGTTTCGGGCTGGGCGGAGCCCGACAGCAACCGC	120	
Qy	121	AGCGCGGCTCGGAGGAGCGCAGCTGGAGCCCGCGGCACATCTCCCGCGGCATCCCGGTC	180	
Db	121	AGCGCGGCTCGGAGGAGCGCAGCTGGAGCCCGCGGCACATCTCCCGCGGCATCCCGGTC	180	
Qy	181	ATCATCACGCGGTCTACTCCGTAGTGTTCGTCTGGGCTTGGTGGGCAATCGCTGGTC	240	
Db	181	ATCATCACGCGGTCTACTCCGTAGTGTTCGTCTGGGCTTGGTGGGCAATCGCTGGTC	240	
Qy	241	ATGTTCTGTGATCATCCGATACACAAAGATGAAGACAGCAACCAATTTTACATATTTAAC	300	

Db 241 ATGTTGCTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAAC 300  
 Qy 301 CTGGCTTTGGCAGATGCTTTAGTTACTACAAACATGCGCTTTTCAGAGTACGGTCTACTTG 360  
 Db 301 CTGGCTTTGGCAGATGCTTTAGTTACTACAAACATGCGCTTTTCAGAGTACGGTCTACTTG 360  
 Qy 361 ATGAATTCCTGCGCTTTTCGGGATGCTGTCGACAGATAGTAATTTCCATTGATTACTAC 420  
 Db 361 ATGAATTCCTGCGCTTTTCGGGATGCTGTCGACAGATAGTAATTTCCATTGATTACTAC 420  
 Qy 421 AACATGTTCCACGACATCTTCCATTTGACCATGATGAGCGTGAGCGGTACATTTGCCGTG 480  
 Db 421 AACATGTTCCACGACATCTTCCATTTGACCATGATGAGCGTGAGCGGTACATTTGCCGTG 480  
 Qy 481 TGCACCCCGTGAAGCTTTTGACCTTCCGACACACCTTGAAGCAAGATCATCAATATC 540  
 Db 481 TGCACCCCGTGAAGCTTTTGACCTTCCGACACACCTTGAAGCAAGATCATCAATATC 540  
 Qy 541 TGCATCTGCTGCTGCTGCTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGCAACCAA 600  
 Db 541 TGCATCTGCTGCTGCTGCTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGCAACCAA 600  
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 Db 661 TGGTGGGACCTTTCAATGAAGATCTCGCTCTTCATCTTTGGCTTCTGATGATCCTGCTC 720  
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 Db 721 ATCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
 Qy 781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGCTGCTGCTGCTGCTG 840  
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 Qy 841 GCAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
 Db 841 GCAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
 Qy 901 AGCACCTCCACAGCAGCTGCTCTCTCCAGCTATTACTTCTGCAATTCCTTTCAGCTAT 960  
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 Qy 961 ACCAAGTAGCTGAAATCCCATCTCTACGCTTTCTTGTATGAAACTTCAAGCGGTCT 1020  
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 Qy 1021 TTCGGGACTTCTGCTTCCACTGAAGATGAGGATGAGCGGAGAGCACTAGCAGATC 1080  
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 Qy 1141 TGACTAGTCTGGA 1154  
 Db 1141 TGACTAGTCTGGA 1154

RESULT 7

ADN30511

ID ADN30511 standard; cDNA; 1154 BP.

XX AC ADN30511;

XX AC

DT 12-AUG-2004 (first entry)

XX Human kappa opioid receptor, hKOR, C856T allele.

DE

XX

KW Human; kappa opioid receptor; hKOR; ss; gene; SNP;  
 KW single nucleotide polymorphism; endogenous opioid system; nociception;  
 KW neurotransmitter release; learning; memory; cognition; pain; cocaine;  
 KW amphetamine; alcohol; tobacco; opiate; withdrawal;  
 KW neuroendocrine function; reproductive function; prolactin regulation;  
 KW stress responsiveness; mood; affect; immune function;  
 KW gastrointestinal function; analgesia; addictive disease;  
 KW chromosome 8q11.2.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT allele replace (846,C)  
 FT /\*tag= a  
 FT /standard\_name= "Single nucleotide polymorphism"  
 XX US2004097704-A1.  
 XX 20-MAY-2004.  
 XX 13-JUL-2001; 2001US-00904584.  
 XX 14-JUL-2000; 2000US-0218300P.  
 XX (KREE/) KREEK M J.  
 XX (YUFE/) YUFEROV V.  
 XX (LAFO/) LAFORGE K S.  
 XX Kreek MJ, Yufarov V, Laforge KS;  
 XX WPI; 2004-389204/36.  
 DR Novel isolated variant allele of human kappa opioid receptor gene, useful  
 XX for determining susceptibility in subject to physiological response,  
 PT condition or disease related to endogenous opioid system.  
 PS Example; SEQ ID NO 7; 29pp; English.  
 XX The invention relates to an isolated variant allele of a human kappa  
 CC opioid receptor gene, comprising a DNA sequence having at least one  
 CC variation in a fully defined wild-type allele of human kappa opioid  
 CC receptor (hKOR) sequence appearing as ADN30505, where the variation  
 CC comprises C852T, C948T, C1008T or their combinations. Also included are  
 CC an isolated nucleic acid molecule selectively hybridizing to the variant,  
 CC a cloning vector comprising the variant and an origin of replication, a  
 CC expression vector comprising the variant associated with a promoter, a  
 CC unicellular host transformed/transfected with the vector and a commercial  
 CC test kit for determining the presence of at least one variation in a hKOR  
 CC gene of an allele in a bodily sample taken from a subject. The hKOR  
 CC variant allele is useful for determining a susceptibility in a subject to  
 CC at least one physiological response, condition or disease related to the  
 CC endogenous opioid system, nociception, neurotransmitter release  
 CC endogenous opioid system, learning, memory, cognition, pain, cocaine,  
 CC amphetamine and other stimulants self-administration, behavioural  
 CC sensitization to cocaine, opiates, alcohol and tobacco, opiate,  
 CC amphetamine and alcohol withdrawal, physical dependence and tolerance;  
 CC neuroendocrine function, reproductive function, prolactin regulation,  
 CC stress responsiveness, physiology and pathology of mood and affect, immune  
 CC function, gastrointestinal function. The hKOR variant allele is useful  
 CC for determining a susceptibility to pain in a subject and is useful for  
 CC determining a therapeutically effective amount of pain reliever to  
 CC administer to a subject in order to induce analgesia in the subject. The  
 CC hKOR variant allele is useful for determining a therapeutically effective  
 CC amount of therapeutic agent to administer to a subject suffering from at  
 CC least one addictive disease to treat the at least one addictive disease.  
 CC The gene for hKOR is located on chromosome 8q11.2. The present sequence  
 CC is the C846T allele of hKOR.  
 XX  
 SQ Sequence 1154 BP; 239 A; 338 C; 287 G; 290 T; 0 U; 0 Other;

Query Match 99.7%; Score 1150.8; DB 12; Length 1154;

Best Local Similarity 99.8%; Pred. No. 1.7e-272;

Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 ATGGAATCCCGATCCAGATCTTCGCGGGAGCGCGCCCTTACCTCGCGCCCGAGCGCC 60
Db |||||
QY 61 TGCCTGCCCCCAACAGCAGCGCTGGTTTCCCGCTGGCGCGAGCCCGACAGCAACGGC 120
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QY 61 TGCCTGCCCCCAACAGCAGCGCTGGTTTCCCGCTGGCGCGAGCCCGACAGCAACGGC 120
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QY 121 AGCGCGCGCTCGGAGGACCGCAGCTGGAGCGCCGACATCTCCCGCGCCATCCCGTGC 180
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QY 121 AGCGCGCGCTCGGAGGACCGCAGCTGGAGCGCCGACATCTCCCGCGCCATCCCGTGC 180
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QY 241 ATGTTCTGGTATCATCCGATACACAAGATGAGACAGCAACCAACATTTACATTTAAC 300
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Db |||||
QY 421 AACATGTTCCACGATCTTACCTTGACCATGATGAGCGTGGACCGTACATTGCCGTG 480
Db |||||
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Db |||||
QY 481 TGCCACCCCGTGAAGGCTTTGAGCTTCGCGACACCCCTTGAAGGCAAGATCATCAATATC 540
Db |||||
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Db |||||
QY 541 TGCATCTGGTGTCTGTCATCTGTGGCATCTCTGCAATAGTCTTTGGAGGACCAAA 600
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Db |||||
QY 601 GTGAGGAGAGCTCGATGATCATGATGATCCTGCGTCTCCAGAGCGTCCGCTCTTTCT 660
Db |||||
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Db |||||
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Db |||||
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Db |||||
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Db |||||
QY 781 GGCTCCCGAGAGAAGATCGCAACCTGGTGGATCACCAGACTGGTCTGGTGGTGGTG 840
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Db |||||
QY 841 GCAGTCTTCGCTGCTCTGCTGACTCCCATTCACATATTCATCTCGTGGAGGCTCTGGG 900
Db |||||
QY 901 AGCACTCTCCACAGCAGCTGCTCTCTCCAGCTATTACTTCTGCAATGCTTAGGCTAT 960
Db |||||
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Db |||||
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Db |||||
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Db |||||
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```
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Db |||||
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Db |||||
QY 1141 TGACTAGTCTGGGA 1154
Db |||||
QY 1141 TGACTAGTCTGGGA 1154
Db |||||

RESULT 8
ADN30509
ID ADN30509 standard; cDNA; 1154 BP.
XX
XX ADN30509;
AC
XX DT 12-AUG-2004 (first entry)
XX
XX Human kappa opioid receptor, hKOR, G36T allele.
DE
XX Human; kappa opioid receptor; hKOR; ss; gene; SNP;
XX single nucleotide polymorphism; endogenous opioid system; nociception;
XX neurotransmitter release; learning; memory; cognition; pain; cocaine;
XX amphetamine; alcohol; tobacco; opiate; withdrawal;
XX neuroendocrine function; reproductive function; prolactin regulation;
XX stress responsivity; mood; affect; immune function;
XX gastrointestinal function; analgesia; addictive disease;
XX chromosome 8q11.2.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX allele replace(36,G)
XX /*tag= a
XX /standard_name= "Single nucleotide polymorphism"
XX
XX US2004097704-A1.
XX
XX 20-MAY-2004.
XX
XX 13-JUL-2001; 2001US-00904584.
XX
XX 14-JUL-2000; 2000US-0218300P.
XX
XX (KREE/) KREEK M J.
XX (YUFE/) YUFEROV V.
XX (LAFO/) LAFORGE K S.
XX
XX Kreek MJ, Yuferov V, Laforge KS;
XX WPI; 2004-389204/36.
XX
XX Novel isolated variant allele of human kappa opioid receptor gene, useful
XX for determining susceptibility in subject to physiological response,
XX condition or disease related to endogenous opioid system.
XX
XX Example; SEQ ID NO 5; 29pp; English.
XX
XX The invention relates to an isolated variant allele of a human kappa
XX opioid receptor gene, comprising a DNA sequence having at least one
XX variation in a fully defined wild-type allele of human kappa opioid
XX receptor (hKOR) sequence appearing as ADN30509, where the variation
XX comprises C952T, C948T, C1008T or their combinations. Also included are
XX an isolated nucleic acid molecule selectively hybridizing to the variant,
XX a cloning vector comprising the variant and an origin of replication, an
XX expression vector comprising the variant associated with a promoter, a
XX unicellular host transformed/transfected with the vector and a commercial
XX test kit for determining the presence of at least one variation in a hKOR
XX gene of an allele in a bodily sample taken from a subject. The hKOR
XX variant allele is useful for determining a susceptibility in a subject to
XX at least one physiological response, condition or disease related to the
XX endogenous opioid system, nociception, neurotransmitter release
XX endogenous opioid system, learning, memory, cognition, pain, cocaine,
XX amphetamine and other stimulants self-administration, behavioural
```

sensitisation to cocaine, opiates, alcohol and tobacco, opiate, amphetamine and alcohol withdrawal, physical dependence and tolerance; neuroendocrine function, reproductive function, prolactin regulation, stress responsivity, physiology and pathology of mood and affect, immune function, gastrointestinal function. The hKOR variant allele is useful for determining a susceptibility to pain in a subject and is useful for determining a therapeutically effective amount of pain reliever to administer to a subject in order to induce analgesia in the subject. The hKOR variant allele is useful for determining a therapeutically effective amount of therapeutic agent to administer to a subject suffering from at least one addictive disease to treat the at least one addictive disease. The gene for hKOR is located on chromosome 8q11.2. The present sequence is the G36T allele of hKOR.

Sequence 1154 BP; 239 A; 339 C; 286 G; 290 T; 0 U; 0 Other;

Query Match 99.7%; Score 1150.8; DB 12; Length 1154;  
 Best Local Similarity 99.8%; Pred. No. 1.7e-272;  
 Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGACTTCCCGATCCAGATCTTCCGCGGAGCCGGGCTTACCTGCGCCCGAGCGCC 60  
 DB 1 ATGACTTCCCGATCCAGATCTTCCGCGGAGCCGGGCTTACCTGCGCCCGAGCGCC 60  
 QY 61 TGCCTGCCCCCAACAGCAGCGCTGGTTCCCGGCTGGCGAGCCCGACAGCAACGCG 120  
 DB 61 TGCCTGCCCCCAACAGCAGCGCTGGTTCCCGGCTGGCGAGCCCGACAGCAACGCG 120  
 QY 121 AGCGCCGGCTCGGAGGACGGCAGCTGGAGCCCGGCGACATCTCCCGCGCCATCCCGGTC 180  
 DB 121 AGCGCCGGCTCGGAGGACGGCAGCTGGAGCCCGGCGACATCTCCCGCGCCATCCCGGTC 180  
 QY 181 ATCATCAGCGGGTCTACTCCGTAGTCTCGTGGGCTTGGTGGCACTCGCTGGTC 240  
 DB 181 ATCATCAGCGGGTCTACTCCGTAGTCTCGTGGGCTTGGTGGCACTCGCTGGTC 240  
 QY 241 ATGTTCTGTGATCATCCGATACACAAAGATGAAGACAGCAACCAATTTACATATTAA 300  
 DB 241 ATGTTCTGTGATCATCCGATACACAAAGATGAAGACAGCAACCAATTTACATATTAA 300  
 QY 301 CTGGCTTGGCAGATGCTTTAGTTACTACAAACATGCGCTTTCAGAGTACGGTCTACTTG 360  
 DB 301 CTGGCTTGGCAGATGCTTTAGTTACTACAAACATGCGCTTTCAGAGTACGGTCTACTTG 360  
 QY 361 ATGAATTCCTGGCTTTGGGATGCTGTCGAAGATAGTAATTTCCATTTGATTACTAC 420  
 DB 361 ATGAATTCCTGGCTTTGGGATGCTGTCGAAGATAGTAATTTCCATTTGATTACTAC 420  
 QY 421 AACATGTTTACACAGCATCTTCACTTGAACATGATGAGCGTGGACCGCTACATTCGCGTG 480  
 DB 421 AACATGTTTACACAGCATCTTCACTTGAACATGATGAGCGTGGACCGCTACATTCGCGTG 480  
 QY 481 TGCCACCCCGTGAAGGCTTTGGATCTTCGCGACACCTTGAAGGCAAGATCATCAATATC 540  
 DB 481 TGCCACCCCGTGAAGGCTTTGGATCTTCGCGACACCTTGAAGGCAAGATCATCAATATC 540  
 QY 541 TGCATCTGGCTGCTGTCATCTCTTGGCATCTCTGCAATAGTCTTTGGAGGACCAAAA 600  
 DB 541 TGCATCTGGCTGCTGTCATCTCTTGGCATCTCTGCAATAGTCTTTGGAGGACCAAAA 600  
 QY 601 GTCAGGAGAGCGTCGATGTCAATGAGTGTCTTGGAGTTCCGAGATGATGACTACTCC 660  
 DB 601 GTCAGGAGAGCGTCGATGTCAATGAGTGTCTTGGAGTTCCGAGATGATGACTACTCC 660  
 QY 661 TGGTGGGACCTTTCATGAGATCTGGCTTTCATCTTGGCTTCGTGATCCCTGTCCTC 720  
 DB 661 TGGTGGGACCTTTCATGAGATCTGGCTTTCATCTTGGCTTCGTGATCCCTGTCCTC 720  
 QY 721 ATCATCATCTGCTGCTACACCTGATGATCTGCTGCTCTCAAGAGCGTCCGGCTCTTTCT 780  
 DB 721 ATCATCATCTGCTGCTACACCTGATGATCTGCTGCTCTCAAGAGCGTCCGGCTCTTTCT 780  
 QY 781 GGCTCCCGAGAGAAAGATCGCAACCTGCTGATGATCAGAGACTGGTCTGCTGGTGGTG 840

DB 781 GGCTCCCGAGAGAAAGATCGCAACCTGCTGATGATCAGAGACTGGTCTGCTGGTGGTG 840  
 QY 841 GCAGTCTTCGCTGCTGCTGGACTCCATTCACATATTCATCTCTGCTGGAGGCTCTGGGG 900  
 DB 841 GCAGTCTTCGCTGCTGCTGGACTCCCATTCACATATTCATCTCTGCTGGAGGCTCTGGGG 900  
 QY 901 AGCACTCCCCACAGCAGCAGCTGCTCTCCAGCTATTTACTTCTGCAATTCCTTAGGCTAT 960  
 DB 901 AGCACTCCCCACAGCAGCAGCTGCTCTCCAGCTATTTACTTCTGCAATTCCTTAGGCTAT 960  
 QY 961 ACCAACAGTACGCTGAATCCCATTTCTACGCCCTTTCTGATGAAAACCTTCAAGCGGTG 1020  
 DB 961 ACCAACAGTACGCTGAATCCCATTTCTACGCCCTTTCTGATGAAAACCTTCAAGCGGTG 1020  
 QY 1021 TTCGGGACTTCTGCTTTTCCACTGAAGATGAGGAGGCGGACAGCAGTACAGAGTC 1080  
 DB 1021 TTCGGGACTTCTGCTTTTCCACTGAAGATGAGGAGGCGGACAGCAGTACAGAGTC 1080  
 QY 1081 CGAAATACAGTTCAAGGATCTGCTTACCTGAGGACATTCGATGGGATGAATAAACAGTA 1140  
 DB 1081 CGAAATACAGTTCAAGGATCTGCTTACCTGAGGACATTCGATGGGATGAATAAACAGTA 1140  
 QY 1141 TGACTAGTCTGGA 1154  
 DB 1141 TGACTAGTCTGGA 1154

RESULT 9  
 ABZ42678  
 ID ABZ42678 standard; DNA; 1182 BP.  
 XX  
 AC ABZ42678;  
 XX  
 DT 04-MAR-2003 (first entry)  
 XX  
 DE Human opioid receptor kappa 1 nucleotide SEQ ID NO:147.  
 XX  
 KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
 KW G protein-coupled receptor modulator; antibody; immune-related disease;  
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;  
 KW immunological-related cell proliferative disease; autoimmune disease;  
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; pain;  
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
 KW ulcer; gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200261087-A2.  
 XX  
 PD 08-AUG-2002.  
 XX  
 PF 19-DEC-2001; 2001WO-US050107.  
 XX  
 PR 19-DEC-2000; 2000US-0257144P.  
 XX  
 PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
 XX  
 PI Burmer GC, Roush CL, Brown JP;  
 XX  
 DR WPI; 2003-046718/04.  
 DR P-PSDB; ABP81832.  
 XX  
 PT New isolated antigenic peptides e.g., for G protein-coupled receptors  
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions  
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or  
 PT autoimmune diseases.  
 XX  
 PS Disclosure; Fig 1; 523pp; English.

XX The present invention describes antigenic peptides (1) comprising: (a)  
 CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
 CC acids. Also described: (1) an assay for the detection of a particular G  
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; or  
 CC and (2) an isolated antibody having high specificity and high affinity or  
 CC avidity for a particular GPCR. (1) can be used as GPCR modulators and in  
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an  
 CC antibody against a particular GPCR, and in the production of specific  
 CC antibodies. The peptides and antibodies are also useful for detecting the  
 CC presence or absence of corresponding GPCRs. The antigenic peptides for  
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for  
 CC treating immune-related diseases, growth-related diseases, cell  
 CC regeneration-related disease, immunological-related cell proliferative  
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,  
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host  
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory  
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,  
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
 CC any other disorder in which GPCRs are involved. The antibodies may be  
 CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode  
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 1182 BP; 245 A; 345 C; 293 G; 299 T; 0 U; 0 Other;

Query Match 99.2%; Score 1144.4; DB 8; Length 1182;  
 Best Local Similarity 99.5%; Pred. No. 6.2e-271;  
 Matches 1148; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGGAATCCCGATCCAGATCTTCGCGGGGAGCGCGCCCTACTCTGCGCCCGAGCGCC 60  
 DB 14 ATGGAATCCCGATCCAGATCTTCGCGGGGAGCGCGCCCTACTCTGCGCCCGAGCGCC 73  
 QY 61 TGCCTGCCCCCAACAGACGCGCTGTGTTTCCCGGCTGGCGCGGACGAGCAACGCGC 120  
 DB 74 TGCCTGCCCCCAACAGACGCGCTGTGTTTCCCGGCTGGCGCGGACGAGCAACGCGC 133  
 QY 121 AGCGCCGGCTCGGAGGAGCGGACGCTGGAGCGCGCGGACATCTCCCGGGCGATCCCGGTC 180  
 DB 134 AGCGCCGGCTCGGAGGAGCGGACGCTGGAGCGCGCGGACATCTCCCGGGCGATCCCGGTC 193  
 QY 181 ATCATACGGCGGTCTACTCGGTAGTGTTCGTCTGGGCTGGGCGCAACTCGCTGCTC 240  
 DB 194 ATCATACGGCGGTCTACTCGGTAGTGTTCGTCTGGGCTGGGCGCAACTCGCTGCTC 253  
 QY 241 ATGTTCTGTATCATCCGATACACAAGATGAAGACAGCAACCAACATTTACATATTTAAC 300  
 DB 254 ATGTTCTGTATCATCCGATACACAAGATGAAGACAGCAACCAACATTTACATATTTAAC 313  
 QY 301 CTGCGCTTGGCAGATGCTTTAGTTACTACACCATGCGCTTTCAGAGTAGCGTCTACTTG 360  
 DB 314 CTGCGCTTGGCAGATGCTTTAGTTACTACACCATGCGCTTTCAGAGTAGCGTCTACTTG 373  
 QY 361 ATGAATTCCTGGCTTTGGGGATGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420  
 DB 374 ATGAATTCCTGGCTTTGGGGATGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 433  
 QY 421 AACATGTTTCAACAGCATCTTTACCTTGACCATGATGAGCGTGGACCGCTACATTGCGGTG 480  
 DB 434 AACATGTTTCAACAGCATCTTTACCTTGACCATGATGAGCGTGGACCGCTACATTGCGGTG 493  
 QY 481 TGCACCCCGTGAAGGCTTTGGACCTTCGGCACACCCCTTGAAGGCAAAAGATCATCAATATC 540  
 DB 494 TGCACCCCGTGAAGGCTTTGGACCTTCGGCACACCCCTTGAAGGCAAAAGATCATCAATATC 553  
 QY 541 TGCACTGCGCTGCTGCTCATCTGTTGGGATCTCTGCAATAGTCTTGGAGGACCAAA 600  
 DB 554 TGCACTGCGCTGCTGCTCATCTGTTGGGATCTCTGCAATAGTCTTGGAGGACCAAA 613

QY 601 GTACGGGAAGACGTCGATGTCATTCAGTGTCTCTTGCAAGTTCCTCCAGATGATGACTACTCC 660  
 DB 614 GTACGGGAAGACGTCGATGTCATTCAGTGTCTCTTGCAAGTTCCTCCAGATGATGACTACTCC 673  
 QY 661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCTTCGTCGTCGTCCTCTCTC 720  
 DB 674 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCTTCGTCGTCGTCCTCTCTC 733  
 QY 721 ATCATCATCTGCTCTCTACACCTCATGATCATCTGCGTCTCTCAAGAGCGTCCGGCTCTCTTCT 780  
 DB 734 ATCATCATCTGCTCTCTACACCTCATGATCATCTGCGTCTCTCAAGAGCGTCCGGCTCTCTTCT 793  
 QY 781 GGCTCCCGAGAGAAGATCGCAACCTCGTAGGATCACACAGACTGGTCTCTGGTGGTGGTG 840  
 DB 794 GGCTCCCGAGAGAAGATCGCAACCTCGTAGGATCACACAGACTGGTCTCTGGTGGTGGTG 853  
 QY 841 GCAGTCTTCGTCGTCCTGAGCTCCCATTCACATATTCATCTCTGCTGGAGGCTCTGGGG 900  
 DB 854 GCAGTCTTCGTCGTCCTGAGCTCCCATTCACATATTCATCTCTGCTGGAGGCTCTGGGG 913  
 QY 901 AGCACTCTCCACAGCAGCTGCTCTCTCCAGCTATTACTTCTGCATTGCTTAGGCTAT 960  
 DB 914 AGCACTCTCCACAGCAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCTTAGGCTAT 973  
 QY 961 ACCAACAGTAGCTGAATCCCATTTCTCTACGCTTTCTTGATGAAAACTTCAAGCGGTGT 1020  
 DB 974 ACCAACAGTAGCTGAATCCCATTTCTCTACGCTTTCTTGATGAAAACTTCAAGCGGTGT 1033  
 QY 1021 TTCGGGACCTTCTGCTTTCCACTGAGGATGAGGCGGACAGACTAGCAGAGTC 1080  
 DB 1034 TTCGGGACCTTCTGCTTTCCACTGAGGATGAGGCGGACAGACTAGCAGAGTC 1093  
 QY 1081 CGAAATACAGTTACAGGATCTGCTTACCTGAGGACATCGATGGGATGAATAAACCACTA 1140  
 DB 1094 CGAAATACAGTTACAGGATCTGCTTACCTGAGGACATCGATGGGATGAATAAACCACTA 1153  
 QY 1141 TGACTAGTCTGGA 1154  
 DB 1154 TGACTAGTCTGGA 1167  
 RESULT 10  
 ID AAD58490 standard; DNA; 1182 BP.  
 XX AAD58490;  
 XX AAD58490;  
 XX 04-DEC-2003 (first entry)  
 DT Human kappa opioid receptor 1 (KOR) DNA.  
 DE Human; neurological disorder; urinary incontinence; gene therapy; cancer;  
 KW kidney disorder; overactive; oversensitive bladder; dysfunction; bladder;  
 KW urethra; overflow urinary incontinence; stress urinary incontinence;  
 KW nervous system; prostatitis; benign prostatic hyperplasia; nephrotrophic;  
 KW kappa opioid receptor 1; KOR; gene; ds.  
 XX Homo sapiens.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 PH CDS 14..1156  
 FT /\*tag= a  
 FT /product= "Human kappa opioid receptor 1 (KOR)"  
 FT /note= "The CDS is referred to as SEQ ID NO:21 in the  
 FT specification"  
 XX WO2003061573-A2.  
 PN 31-JUL-2003.  
 PD 16-JAN-2003; 2003WO-US001450.  
 XX 18-JAN-2002; 2002US-0349511P.









polynucleotide probes comprising a sequence selected from one of the 1490 sequences mentioned in the specification. The combination is useful as an array element in a microarray for monitoring the expression of a number of target polynucleotides. The microarray is particularly useful in the diagnosis and treatment of cancer and immunopathology and neuropathology. The microarray is useful in diagnostics and treatment regimens, drug discovery and development, toxicological and carcinogenicity studies, forensics and pharmacogenomics. The microarray is also useful for monitoring progression of diseases and for developing sophisticated profiles for the effects of currently available therapeutic drugs. The combination is also useful for purifying a subpopulation of mRNAs, cDNAs and genomic fragments and in research and diagnostic applications. The array can detect changes in expression in a large number of genes coding for different signaling pathway populations which can be used to diagnose various diseases including cancer e.g. adenocarcinoma and leukaemia immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease and Parkinson's disease. The present sequence represents a polynucleotide probe of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=06500938B1

Sequence 1182 BP; 245 A; 345 C; 293 G; 299 T; 0 U; 0 Other;

Query Match 99.2%; Score 1144.4; DB 10; Length 1182;  
Best Local Similarity 99.5%; Pred. No. 6.2e-271;  
Matches 1148; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

1 ATGGATCTCCCGATCCAGATCTTCCGGGGAGCGCGGCTTACCTTGGCGCCCGAGCGCC 60  
14 ATGGAATCCCGATTCAGATCTTCCCGGGAGCTGGCCCTACCTTGGCGCCCGAGCGCC 73  
61 TGCCTGCCCGCCCAACAGAGCGCTGTTCCCGGCTGGCGGAGCCCGACAGCAACGGC 120  
74 TGCCTGCCCGCCCAACAGAGCGCTGTTCCCGGCTGGCGGAGCCCGACAGCAACGGC 133  
121 AGCGCGGCTCGGAGGACGCGAGCTGGAGCGCGCACATCTCCCGCGCATCCCGGTC 180  
134 AGCGCGGCTCGGAGGACGCGAGCTGGAGCGCGCACATCTCCCGCGCATCCCGGTC 193  
181 ATCATCAGCGGCTTACTCCGAGTGTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 240  
194 ATCATCAGCGGCTTACTCCGAGTGTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 253  
241 ATCTTCGTGATCATCCGATACAAAGATGAACAGCAACCAACATTTACATATTAAAC 300  
254 ATGTTGATGATCCGATACAAAGATGAACAGCAACCAACATTTACATATTAAAC 313  
301 CTGGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCCCTTTTCAGAGTACGGTCTATTG 360  
314 CTGGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCCCTTTTCAGAGTACGGTCTATTG 373  
361 ATGAATCTCGGCTTTGGGAGTGTGTGCAAGATAGTAAATTTCCATTTGATTACTAC 420  
374 ATGAATCTCGGCTTTGGGAGTGTGTGCAAGATAGTAAATTTCCATTTGATTACTAC 433  
421 AACATGTTCCAGAGCTTTCACCTTGACCATGATGAGCGTGACCGCTACATTTGCGGTG 480  
434 AACATGTTCCAGAGCTTTCACCTTGACCATGATGAGCGTGACCGCTACATTTGCGGTG 493  
481 TGCACCCCGTGAAGGCTTTGGAGTTCCTCCGACACACCCCTTGAAGGCAAGATCATCAATATC 540  
494 TGCACCCCGTGAAGGCTTTGGAGTTCCTCCGACACACCCCTTGAAGGCAAGATCATCAATATC 553  
541 TGCAATCTGGCTGTGTCGTCATCTGTTGGATCTCTGCAATAGTCTCTTGGAGGACCAAA 600  
554 TGCAATCTGGCTGTGTCGTCATCTGTTGGATCTCTGCAATAGTCTCTTGGAGGACCAAA 613  
601 GTGAGGAGAGAGCTTCGATGTCATTGAGTGTCTCTGAGTTCAGATGATGATGATCTCC 660  
614 GTGAGGAGAGAGCTTCGATGTCATTGAGTGTCTCTGAGTTCAGATGATGATGATCTCC 673  
661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTTGCCTTCGTGATCCCTGTCCTC 720

674 TGGTGGGACCTCTTTCATGAAGATCTGCGTCTTTCATCTTTGCGCTTCGTGATCCCTGTCCTC 733  
721 ATCATCATCTGCTGTACACCTCGATGATCCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780  
734 ATCATCATCTGCTGTACACCTCGATGATCCCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 793  
781 GGCTCCCGAGAGAAAGATCGCAACCTGCTAGGATCACCAGACTGCTGCTGCTGCTGGTG 840  
794 GGCTCCCGAGAGAAAGATCGCAACCTGCTAGGATCACCAGACTGCTGCTGCTGCTGGTG 853  
841 GGAGTCTTCTGCTGTGTGAGTCTCCATTCATCATATTCATCTGCTGAGGCTCTGGGG 900  
854 GCGGTTTCTGCTGTGTGAGTCTCCATTCATCATATTCATCTGCTGAGGCTCTGGGG 913  
901 AGCACCCTCCAGACAGACTGCTCTCTCCAGTCTTCTGCTGCTGCTGCTGCTGCTGCTAT 960  
914 AGCACCCTCCAGACAGACTGCTCTCTCCAGTCTTCTGCTGCTGCTGCTGCTGCTGCTAT 973  
961 ACCAAGTAGCTGATCCCATCTCTACGCTTCTTGTGATGAAATCTTCAAGCGGTGT 1020  
974 ACCAAGTAGCTGATCCCATCTCTACGCTTCTTGTGATGAAATCTTCAAGCGGTGT 1033  
1021 TTCCGGGACTTCTGCTTCCACTGAAAGATGAGATGAGAGCGGCGAGCACTAGCAGATC 1080  
1034 TTCCGGGACTTCTGCTTCCACTGAAAGATGAGATGAGAGCGGCGAGCACTAGCAGATC 1093  
1081 CGAAATACAGTTTCAGATCTCTGCTTACCTGAGGACATCGATGGGATGAATAACCACTA 1140  
1094 CGAAATACAGTTTCAGATCTCTGCTTACCTGAGGACATCGATGGGATGAATAACCACTA 1153  
1141 TGACTAGTCTGTGA 1154  
1154 TGACTAGTCTGTGA 1167  
RESULT 13  
ADI56615  
ID ADI56615 standard; DNA; 1182 BP.  
XX ADI56615;  
XX ADI56615;  
XX 22-APR-2004 (first entry)  
XX Human polynucleotide probe #1417.  
XX Human; probe; ss; receptor-like polypeptide; transducing polypeptide;  
XX effector-like polypeptide; cancer; immunopathology; neuropathology;  
XX drug development; toxicology; carcinogenicity;  
XX signalling pathway polypeptide; adrenal gland; bladder; bone;  
XX bone marrow; brain; breast; cervix; tumour; immunopathology; AIDS;  
XX diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology;  
XX dementia; amnesia; epilepsy; Alzheimer's disease; depression.  
XX Homo sapiens.  
XX US2004010136-A1.  
XX 15-JAN-2004.  
XX 26-NOV-2002; 2002US-00305720.  
XX 30-JAN-1998; 98US-00016434.  
XX (INCY-) INCYTE GENOMICS INC.  
XX Au-Young J, Seilhamer JJ;  
XX WPI; 2004-090520/09.  
XX New composition comprising polynucleotide probes, useful as array  
XX elements in a microarray for monitoring the expression of target  
XX polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic





PN WO9601898-A1.  
XX  
PD 25-JAN-1996.  
XX  
PF 07-JUL-1995; 95WO-FR000912.  
XX  
PR 11-JUL-1994; 94PR-00008531.  
XX  
PA (UYST-) UNIV PASTEUR STRASBOURG LOUIS.  
XX  
PI Kieffer B., Simonin F;  
XX  
XX WPI; 1996-097628/10.  
DR P-PSDB; AAR88722.  
DR  
XX  
XX New nucleic acid encoding the human Kappa opioid receptor - useful in  
PT diagnosis and therapy, and for isolating receptor ligands and modulators.  
PT  
XX  
XX Claim 3; Page 13-15; 30pp; French.  
XX  
XX This sequence codes for the human kappa opioid receptor and was obtained  
CC from two overlapping cDNA fragments isolated from a human placental cDNA  
CC library. The fragments were amplified from the library using PCR primers  
CC based on the sequence of human genomic clones which hybridised with a  
CC murine delta receptor cDNA probe. Nucleotide probes derived from the  
CC kappa opioid receptor coding sequence are useful for diagnosis of  
CC neurological, cardio- vascular and psychiatric disorders associated with  
CC opioid receptors  
XX  
XX Sequence 1142 BP; 236 A; 337 C; 283 G; 286 T; 0 U; 0 Other;  
SQ

Query Match 98.8%; Score 1140.4; DB 2; Length 1142;  
Best Local Similarity 99.9%; Pred. No. 5.9e-270;  
Matches 1141; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGACTCCCCGATCCAGATCTTCGGGGAGAGCGGGCCCTACTCTGGCCCCCGAGGCC 60  
Db |||||  
Qy 1 ATGACTCCCCGATCCAGATCTTCGGGGAGAGCGGGCCCTACTCTGGCCCCCGAGGCC 60  
Db |||||  
Qy 61 TGCCTGCCCCCAACAGCAGCGGCTGTTTCCCGCTGGGCGGAGCCCGACAGCAACGGC 120  
Db |||||  
Qy 61 TGCCTGCCCCCAACAGCAGCGGCTGTTTCCCGCTGGGCGGAGCCCGACAGCAACGGC 120  
Db |||||  
Qy 121 AGCCCGGCTCGGAGGACGGCAGCTGGAGCCCGCAGCATCTCCCGGCCCATCCCGGTC 180  
Db |||||  
Qy 121 AGCCCGGCTCGGAGGACGGCAGCTGGAGCCCGCAGCATCTCCCGGCCCATCCCGGTC 180  
Db |||||  
Qy 181 ATCATCAGCGGGTCTACTCGTAGTGTTCGTCTGGGCTGGTGGGCAACTCGCTGGTC 240  
Db |||||  
Qy 181 ATCATCAGCGGGTCTACTCGTAGTGTTCGTCTGGGCTGGTGGGCAACTCGCTGGTC 240  
Db |||||  
Qy 241 ATGTTCTGTATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATTTAAC 300  
Db |||||  
Qy 241 ATGTTCTGTATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATTTAAC 300  
Db |||||  
Qy 301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACTGCCCCCTTTCAGAGTAGGCTACTTG 360  
Db |||||  
Qy 301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACTGCCCCCTTTCAGAGTAGGCTACTTG 360  
Db |||||  
Qy 361 ATGAATTCCTGGCCCTTTTGGGGATGCTGTGCAAGATAGTAATTTCAATGTATATAC 420  
Db |||||  
Qy 361 ATGAATTCCTGGCCCTTTTGGGGATGCTGTGCAAGATAGTAATTTCAATGTATATAC 420  
Db |||||  
Qy 421 AACATGTTCCACGATCTTACCTTCACCATGATGAGCGGTGGACCGCTACATTCGCGTG 480  
Db |||||  
Qy 421 AACATGTTCCACGATCTTACCTTCACCATGATGAGCGGTGGACCGCTACATTCGCGTG 480  
Db |||||  
Qy 481 TGCCACCCCGTGAAGGCTTTGGACTTCGGACACCTTTGAAGGCAAGATCATCAATATC 540  
Db |||||  
Qy 481 TGCCACCCCGTGAAGGCTTTGGACTTCGGACACCTTTGAAGGCAAGATCATCAATATC 540  
Db |||||  
Qy 541 TGCATCTGGCTGCTCGTCAATCTGTTGGCATCTCTGCAATAGTCTTGGAGGCCACCAA 600  
Db |||||

541 TGCATCTGGCTGCTCGTCAATCTGTTGGCATCTCTGCAATAGTCTTGGAGGCCACCAA 600  
601 GTCAGGGAAGACGTCGATGTCATTGAGTGTCTCTTGCAGTTCCTCCAGATGATGACTACTCC 660  
601 GTCAGGGAAGACGTCGATGTCATTGAGTGTCTCTTGCAGTTCCTCCAGATGATGACTACTCC 660  
661 TGGTGGGACCTCTTTCATGAAGATCTGGGTCTTCATCTTGGCTTTCGTGATCCCTGTCTC 720  
661 TGGTGGGACCTCTTTCATGAAGATCTGGGTCTTCATCTTGGCTTTCGTGATCCCTGTCTC 720  
721 ATCATCATCTGCTGTACACCCCTGATGATCTGGGTCTCAAGAGCGTCCGCTCTCTTCT 780  
721 ATCATCATCTGCTGTACACCCCTGATGATCTGGGTCTCAAGAGCGTCCGCTCTCTTCT 780  
781 GGGTCCCGAGAGAAAGATCGCAACTCGTAGGATCACAGACTGGTCTCTGTTGGTGTG 840  
781 GGGTCCCGAGAGAAAGATCGCAACTCGTAGGATCACAGACTGGTCTCTGTTGGTGTG 840  
841 GCAGTCTTCTGCTGCTGCTGCACTCCCATTCACATATTCATCTCTGGTGGAGGCTCTGGGG 900  
841 GCAGTCTTCTGCTGCTGCTGCACTCCCATTCACATATTCATCTCTGGTGGAGGCTCTGGGG 900  
901 AGCACCTCCACAGACAGCTGCTCTCTCCAGCTATTACTTTCGATTCGCTTAGGCTAT 960  
901 AGCACCTCCACAGACAGCTGCTCTCTCCAGCTATTACTTTCGATTCGCTTAGGCTAT 960  
961 ACCAAACAGTAGCTGAATCCCATCTCTACGCTTCTTGTATGAAACTTCAAGCGGTGT 1020  
961 ACCAAACAGTAGCTGAATCCCATCTCTACGCTTCTTGTATGAAACTTCAAGCGGTGT 1020  
1021 TTCGGGACTTCTGCTTTCACCTGAAGATGAGGATGGAGCGGCAGAGCACTAGCAGAGTC 1080  
1021 TTCGGGACTTCTGCTTTCACCTGAAGATGAGGATGGAGCGGCAGAGCACTAGCAGAGTC 1080  
1081 CGAAATACAGTTACAGGATCTCTGCTTACCTGAGGACATCGATGGGATGAATAAACCAAGTA 1140  
1081 CGAAATACAGTTACAGGATCTCTGCTTACCTGAGGACATCGATGGGATGAATAAACCAAGTA 1140  
1141 TG 1142  
1141 TG 1142

Search completed: April 6, 2005, 13:53:15  
Job time : 703.667 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 6, 2005, 12:28:42 ; Search time 215 Seconds  
(without alignments)  
8782.620 Million cell updates/sec

Title: US-09-904-584-3

Perfect score: 1154

Sequence: 1 atgagcccccgcagccagat.....ccagatgactagtcgtgga 1154

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_NA.\*

- 1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*
- 2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1144.4	99.2	1182	4	US-09-016-434-1417
2	1141.4	98.9	1143	4	US-09-341-446B-1
3	1140.4	98.8	1142	3	US-08-765-743-1
4	1136.2	98.5	1284	4	US-09-341-446B-3
5	1130.2	97.9	1143	4	US-09-826-509-542
6	999.4	86.6	1275	4	US-09-341-446B-5
7	994.6	86.2	1275	4	US-09-341-446B-7
8	912.4	79.1	1408	4	US-09-214-904-5
9	912.4	79.1	1410	3	US-08-147-592A-1
10	869.6	75.4	1000	3	US-08-147-592A-11
11	869.6	75.4	1000	3	US-08-292-694A-11
12	869.6	75.4	1000	3	US-08-430-286A-1
13	448	38.8	1618	3	US-08-889-108-1
14	448	38.8	1618	3	US-08-889-108-3
15	448	38.8	1618	3	US-08-889-108-7
16	448	38.8	1618	3	US-08-120-601B-1
17	448	38.8	1618	3	US-08-120-601B-3
18	448	38.8	1618	5	PCT-US94-10358-1
19	448	38.8	1618	5	PCT-US94-10358-3
20	436.4	37.8	1610	3	US-08-889-108-7
21	436.4	37.8	1610	5	PCT-US94-10358-7
22	436.4	37.8	1610	3	US-08-188-275A-1
23	436.4	37.8	1610	3	US-09-351-198-1
24	436.4	37.8	2162	3	US-09-113-426-1
25	436.4	37.8	2162	4	US-09-016-434-1379
26	436.4	37.8	2162	4	US-09-355-709C-7
27	434	37.6	1334	4	US-09-761-962A-3

Sequence 11, Appl  
Sequence 1, Appl  
Sequence 16, Appl  
Sequence 9, Appl  
Sequence 10, Appl  
Sequence 546, App  
Sequence 544, App  
Sequence 1, Appl  
Sequence 4, Appl  
Sequence 15, Appl  
Sequence 15, Appl  
Sequence 1, Appl  
Sequence 7, Appl  
Sequence 7, Appl  
Sequence 3, Appl  
Sequence 1, Appl  
Sequence 3, Appl  
Sequence 3, Appl

#### ALIGNMENTS

RESULT 1  
US-09-016-434-1417  
; Sequence 1417, Application US/09016434  
; Patent No. 6500938  
; GENERAL INFORMATION:  
; APPLICANT: Janice Au-Young  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1490  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/016,434  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0002 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 1417:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1182 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: 9532059  
US-09-016-434-1417

Query Match 99.2%; Score 1144.4; DB 4; Length 1182;  
Best Local Similarity 99.5%; Pred. No. 7.4e-284;



Matches 1148; Conservative 0; Mismatches 6; Indels 0; Gaps 0;			
QY	1	ATGGACTCCCGATCCAGATCTTCCGGGGAGCGGGCCCTACCTGCGCCCGAGCGCC	60
DB	14	ATGGAATCCCGGATTCAGATCTTCCGGGGAGCGCTGGCCCTACCTGCGCCCGAGCGCC	73
QY	61	TGCTCTGCCCCCAACAGACGCGCTGGTTTCCGGCTGGGGCCGAGCCCGACAGCAACCGC	120
DB	74	TGCTCTGCCCCCAACAGACGCGCTGGTTTCCGGCTGGGGCCGAGCCCGACAGCAACCGC	133
QY	121	AGCGCGGCTCGAGACGCGAGCTGGAGCGCGCGACATCTCCCGGCCATTCGCGGTC	180
DB	134	AGCGCGGCTCGAGAGCGCGAGCTGGAGCGCGCGACATCTCCCGGCCATTCGCGGTC	193
QY	181	ATCATCACGGCGCTTACTCCGCTAGTGTTCGTGGGCTTGGTGGCAACTCGCTGTC	240
DB	194	ATCATCACGGCGCTTACTCCGCTAGTGTTCGTGGGCTTGGTGGCAACTCGCTGTC	253
QY	241	ATGTTCTGATCATCCGATACACAAAGATGAAGACAGCAACCAATTTACATATTAAAC	300
DB	254	ATGTTCTGATCATCCGATACACAAAGATGAAGACAGCAACCAATTTACATATTAAAC	313
QY	301	CTGGCTTTGGCAGATGCTTAGTTACTACAAACATGCCCTTTACAGAGTACGGTCTACTTG	360
DB	314	CTGGCTTTGGCAGATGCTTAGTTACTACAAACATGCCCTTTACAGAGTACGGTCTACTTG	373
QY	361	ATGAATTCCTGGCTTTGGGGATGCTGTCGAAGATAGTAAATTTCCATTTGATTAATAC	420
DB	374	ATGAATTCCTGGCTTTGGGGATGCTGTCGAAGATAGTAAATTTCCATTTGATTAATAC	433
QY	421	AACATGTTTACACAGCATCTTACCTTGACCATGATGAGCGTGACCGCTACATTTGCCGTG	480
DB	434	AACATGTTTACACAGCATCTTACCTTGACCATGATGAGCGTGACCGCTACATTTGCCGTG	493
QY	481	TGCCACCCCGTGAAGCTTTGGACTTCGCGACACCCCTTGAAGCAAAAGATCATCAATATC	540
DB	494	TGCCACCCCGTGAAGCTTTGGACTTCGCGACACCCCTTGAAGCAAAAGATCATCAATATC	553
QY	541	TGCATCTGGCTGCTGCTCATCTGTTGGCATCTTGCAATGCTCTTGGAGGACACAA	600
DB	554	TGCATCTGGCTGCTGCTCATCTGTTGGCATCTTGCAATGCTCTTGGAGGACACAA	613
QY	601	GTGAGGGAAGACGTCGATGTCATTGAGTGTCTCTTCAGGTTCCAGATGATGACTACTCC	660
DB	614	GTGAGGGAAGACGTCGATGTCATTGAGTGTCTCTTCAGGTTCCAGATGATGACTACTCC	673
QY	661	TGTTGGGACCTCTTCAATGAAGATCTGGCTTTCATCTTTGGCTTCTGATCCCTGCTTC	720
DB	674	TGTTGGGACCTCTTCAATGAAGATCTGGCTTTCATCTTTGGCTTCTGATCCCTGCTTC	733
QY	721	ATCATCATCTGCTGCTACACCTGATGATCTCGCTCTCAAGAGCGTCCGGCTCTCTTCT	780
DB	734	ATCATCATCTGCTGCTACACCTGATGATCTCGCTCTCAAGAGCGTCCGGCTCTCTTCT	793
QY	781	GGCTCCCGAGAGAAAGATCGCAACCTCGTAGGATCACAGACTGGTCTGTTGGTGGTG	840
DB	794	GGCTCCCGAGAGAAAGATCGCAACCTCGTAGGATCACAGACTGGTCTGTTGGTGGTG	853
QY	841	GCAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	900
DB	854	GCAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	913
QY	901	AGCACTCTCCACAGCAGCTGCTCTCTCCAGCTATTACTTCTGCAATTTGCTTAGGCTAT	960
DB	914	AGCACTCTCCACAGCAGCTGCTCTCTCCAGCTATTACTTCTGCAATTTGCTTAGGCTAT	973
QY	961	ACCAACAGTAGCTGTAATCCCATTTCTACGCTTTCTTGATGAAATTTCAAGCGGTGT	1020
DB	974	ACCAACAGTAGCTGTAATCCCATTTCTACGCTTTCTTGATGAAATTTCAAGCGGTGT	1033
QY	1021	TTCCGGGACTCTGCTTTTCACTAGATGAGATGGAGCGGCGAGGACTAGCAGATC	1080
DB	1034	TTCCGGGACTCTGCTTTTCACTAGATGAGATGGAGCGGCGAGGACTAGCAGATC	1093

QY	1081	CGAAATACAGTTCCAGATCTTACCTTACCTGAGGACATCGATGGATGAATAAACAGTA	1140
DB	1094	CGAAATACAGTTCCAGATCTTACCTTACCTGAGGACATCGATGGATGAATAAACAGTA	1153
QY	1141	TCAGTGTGCTGGA	1154
DB	1154	TGACTAGTGTGGA	1167

RESULT 2

US-09-341-446B-1  
; Sequence 1, Application US/09341446B  
; Patent No. 6518480  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Bruce R.  
; TITLE OF INVENTION: Selective Target Cell Activation By  
; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated  
; TITLE OF INVENTION: Superiorly By Synthetic Ligand  
; FILE REFERENCE: UCAL-049CIP  
; CURRENT APPLICATION NUMBER: US/09/341,446B  
; CURRENT FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US97/05334  
; PRIOR FILING DATE: 1997-03-25  
; PRIOR APPLICATION NUMBER: US 08/622,348  
; PRIOR FILING DATE: 1996-03-26  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1143  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-341-446B-1

Query Match 98.9%; Score 1141.4; DB 4; Length 1143;  
Best Local Similarity 99.9%; Pred. No. 4.3e-283;  
Matches 1142; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	ATGGACTCCCGATCCAGATCTTCCGGGGAGCGGGCCCTACCTGCGCCCGAGCGCC	60
DB	1	ATGGACTCCCGATCCAGATCTTCCGGGGAGCGGGCCCTACCTGCGCCCGAGCGCC	60
QY	61	TGCTCTGCCCCCAACAGACGCGCTGGTTTCCGGCTGGGGCCGAGCCCGACAGCAACCGC	120
DB	61	TGCTCTGCCCCCAACAGACGCGCTGGTTTCCGGCTGGGGCCGAGCCCGACAGCAACCGC	120
QY	121	AGCGCGGCTCGAGAGCGCGAGCTGGAGCCCGGCACATCTCCCGGCCATCCCGGTC	180
DB	121	AGCGCGGCTCGAGAGCGCGAGCTGGAGCCCGGCACATCTCCCGGCCATCCCGGTC	180
QY	181	ATCATCACGGCGCTTACTCCGCTAGTGTTCGTGGGCTTGGTGGGCAACTCGCTGGTC	240
DB	181	ATCATCACGGCGCTTACTCCGCTAGTGTTCGTGGGCTTGGTGGGCAACTCGCTGGTC	240
QY	241	ATGTTCTGATCATTCGGATACAAAGATGAAGACAGCAACCAATTTACATATTAAAC	300
DB	241	ATGTTCTGATCATTCGGATACAAAGATGAAGACAGCAACCAATTTACATATTAAAC	300
QY	301	CTGGCTTTGGCAGATGCTTTAGTTACTACCAACATGCTCTTCCAGAGTACGGTCTACTTG	360
DB	301	CTGGCTTTGGCAGATGCTTTAGTTACTACCAACATGCTCTTCCAGAGTACGGTCTACTTG	360
QY	361	ATGAATTCCTGGCTTTGGGGATGCTGTGCAAGATAGTAAATTTCCATTTGATTAATAC	420
DB	361	ATGAATTCCTGGCTTTGGGGATGCTGTGCAAGATAGTAAATTTCCATTTGATTAATAC	420
QY	421	AACATGTTTACACAGCATCTTACCTTGACCATGATGAGCGTGACCGCTACATTTGGCGTG	480
DB	421	AACATGTTTACACAGCATCTTACCTTGACCATGATGAGCGTGACCGCTACATTTGGCGTG	480
QY	481	TGCCACCCCGTGAAGCTTTGGACTTCGCGACACCCCTTGAAGCAAAAGATCATCAATATC	540
DB	481	TGCCACCCCGTGAAGCTTTGGACTTCGCGACACCCCTTGAAGCAAAAGATCATCAATATC	540



QY 661 TGGTGGGACCTTTCATGAGATCTGCGTCTTCATCTTTGCTTCGTGATCCCTGTCCTC 720  
DB 661 TGGTGGGACCTTTCATGAGATCTGCGTCTTCATCTTTGCTTCGTGATCCCTGTCCTC 720  
QY 721 ATCATCATCTGCTGTACACCTCGATGATCTCGGTCTCAAGAGCGTCCGGCTCCTTTCT 780  
DB 721 ATCATCATCTGCTGTACACCTCGATGATCTCGGTCTCAAGAGCGTCCGGCTCCTTTCT 780  
QY 781 GGTCTCCGAGAGAAAGATGCAACCTGCGTGGATCACCAGACTGCTGCTGCTGCTGCTG 840  
DB 781 GGTCTCCGAGAGAAAGATGCAACCTGCGTGGATCACCAGACTGCTGCTGCTGCTGCTG 840  
QY 841 GCAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
DB 841 GCAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
QY 901 AGACCTCCACAGCAGCTGCTCTCTCCAGCTATTAATTCCTGATTCCTGCTGCTGCTG 960  
DB 901 AGACCTCCACAGCAGCTGCTCTCTCCAGCTATTAATTCCTGATTCCTGCTGCTGCTG 960  
QY 961 ACCAACAGTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020  
DB 961 ACCAACAGTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020  
QY 1021 TTCCGGGACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080  
DB 1021 TTCCGGGACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080  
QY 1081 CGAAATACAGTTACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
DB 1081 CGAAATACAGTTACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
QY 1141 TG 1142  
DB 1141 TG 1142

RESULT 4

US-09-341-446B-3  
; Sequence 3, Application US/09341446B  
; Patent No. 6518480  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Bruce R.  
; TITLE OF INVENTION: Selective Target Cell Activation By  
; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated  
; TITLE OF INVENTION: Superiorly By Synthetic Ligand  
; FILE REFERENCE: UCAL-04SCIP  
; CURRENT APPLICATION NUMBER: US/09/341,446B  
; CURRENT FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US97/05334  
; PRIOR FILING DATE: 1997-03-25  
; PRIOR APPLICATION NUMBER: US 08/622,348  
; PRIOR FILING DATE: 1996-03-26  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1284  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: modified KOR  
US-09-341-446B-3

Query Match 98.5%; Score 1136.2; DB 4; Length 1284;  
Best Local Similarity 99.7%; Pred. No. 9.8e-282;  
Matches 1138; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 TGGACTCCCGATCCAGATCTTCCGGGGGAGCGGGCCCTACTGCGGCCCGAGCGCCT 61  
DB 113 TCAGCTCCCGATCCAGATCTTCCGGGGGAGCGGGCCCTACTGCGGCCCGAGCGCCT 172  
QY 62 GCTTGGCCCCCAACAGCAGCGCTGTTTCCGGGCTGGGCGGAGCGCGAGCAAGCGCA 121

DB 173 GCGTCCCCCAACAGCAGCGCTGTTTCCGGGCTGGGCGGAGCCCGAGCAACGGCA 232  
QY 122 GCGCGGCTCGAGGAGCGGAGCTGGAGCCGCGCACATCTCCCGGCCATCCCGGCTCA 181  
DB 233 GCGCGGCTCGAGGAGCGGAGCTGGAGCCGCGCACATCTCCCGGCCATCCCGGCTCA 292  
QY 182 TCATCAGCGGCTCTACTCCGTAAGTTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 241  
DB 293 TCATCAGCGGCTCTACTCCGTAAGTTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 352  
QY 242 TGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 301  
DB 353 TGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 412  
QY 302 TGGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCTTTTTCAGAGTACGCTTACTTGA 361  
DB 413 TGGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCTTTTTCAGAGTACGCTTACTTGA 472  
QY 362 TGAATTCCTGGGCTTTTGGGGATGCTGCTGCAAGATAGTAATTTCCATTGATTACTACA 421  
DB 473 TGAATTCCTGGGCTTTTGGGGATGCTGCTGCAAGATAGTAATTTCCATTGATTACTACA 532  
QY 422 ACATGTTTACACAGCATCTTACCTTGACCATGATGAGCGTGGACCGCTACATTCGCGTGT 481  
DB 533 ACATGTTTACACAGCATCTTACCTTGACCATGATGAGCGTGGACCGCTACATTCGCGTGT 592  
QY 482 GCCACCCGCTGAAGGCTTTGGGACTTCCGACACCCCTTGAAGGCAAGATCATCAATATCT 541  
DB 593 GCCACCCGCTGAAGGCTTTGGGACTTCCGACACCCCTTGAAGGCAAGATCATCAATATCT 652  
QY 542 GCATCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 601  
DB 653 GCATCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 712  
QY 602 TCAGGGAAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 661  
DB 713 TCAGGGAAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 772  
QY 662 GGTGGGACCTTTCATGAGATCTGCTGCTTTCATCTTTGCTTTCGTGATCCCTGCTCTCA 721  
DB 773 GGTGGGACCTTTCATGAGATCTGCTGCTTTCATCTTTGCTTTCGTGATCCCTGCTCTCA 832  
QY 722 TCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 781  
DB 833 TCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 892  
QY 782 GCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACAGACTGGTCTGCTGCTGCTGCTG 841  
DB 893 GCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACAGACTGGTCTGCTGCTGCTGCTG 952  
QY 842 CAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 901  
DB 953 CAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1012  
QY 902 GCACCTCCACAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 961  
DB 1013 GCACCTCCACAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1072  
QY 962 CCACAGTAGGCTGATCCCATCTCTACGCTTTTCTTGGTGAAGAACTTTCAAGCGGTGTT 1021  
DB 1073 CCACAGTAGGCTGATCCCATCTCTACGCTTTTCTTGGTGAAGAACTTTCAAGCGGTGTT 1132  
QY 1022 TCCGGGACTTCTGCTTTTCCACTGAAGATGAGGATGGAGCGGAGAGCACTAGCAGAGTCC 1081  
DB 1133 TCCGGGACTTCTGCTTTTCCACTGAAGATGAGGATGGAGCGGAGAGCACTAGCAGAGTCC 1192  
QY 1082 GAAATACAGTTTTCAGGATCTGCTTCTCAGGAGATTCAGTGGATGAATAAACAGTAT 1141  
DB 1193 GAAATACAGTTTTCAGGATCTGCTTCTCAGGAGATTCAGTGGATGAATAAACAGTAT 1252  
QY 1142 G 1142  
DB 1253 G 1253

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RESULT 5
US-09-826-509-542
; Sequence 542, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Protein-Coupled Receptors
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 542
; LENGTH: 1143
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-509-542

Query Match      97.9%; Score 1130.2; DB 4; Length 1143;
Best Local Similarity 99.3%; Pred. No. 3.2e-280;
Matches 1135; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ATGACTCCCCGATCCAGATCTTCGGGGGAGCGCGGCCCTACTCGGCCCGGAGCGCC 60
Db 1 ATGGAATCCCCGATCCAGATCTTCGGGGGAGCGCGGCCCTACTCGGCCCGGAGCGCC 60
Qy 61 TGCCTGCCCCCACCAGAGCGCTGTTTCCCGGCTGGGCGGAGCGCCGACAGCAAGCGC 120
Db 61 TGCCTGCCCCCACCAGAGCGCTGTTTCCCGGCTGGGCGGAGCGCCGACAGCAAGCGC 120
Qy 121 AGCGCCGGCTCGGAGGAGCGCGAGCTGAGCGCCGCGACATCTCCCGGCCATCCCGGTC 180
Db 121 AGCGCCGGCTCGGAGGAGCGCGAGCTGAGCGCCGCGACATCTCCCGGCCATCCCGGTC 180
Qy 181 ATCATCAGCGCGTCTACTCCGTAGTGTTCGTGCGGCTTGGTGGCAACTCGCTGGTC 240
Db 181 ATCATCAGCGCGTCTACTCCGTAGTGTTCGTGCGGCTTGGTGGCAACTCGCTGGTC 240
Qy 241 ATGTTCTGTGATCATCCGATACACAAAGATGAGACAGCAACCAATTTACATTTAAC 300
Db 241 ATGTTCTGTGATCATCCGATACACAAAGATGAGACAGCAACCAATTTACATTTAAC 300
Qy 301 CTGCTTTTGGCAGATGCTTTAGTTTACTACAAACCATGCCCTTTCAGAGTACGCTACTTG 360
Db 301 CTGCTTTTGGCAGATGCTTTAGTTTACTACAAACCATGCCCTTTCAGAGTACGCTACTTG 360
Qy 361 ATGAATCTCTGGCCTTTTGGGAGTGTCTGTCAGAGTAGTAATTTCCATTGATTAAC 420
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Db 421 AACATGTTTACCAGCATCTTACCTTGACCATGATGAGCGTGGACCGCTACATTTGCCGTG 480
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Qy 541 TGCACTCTGGTGTCTGCTCATCTGTGTTGGCATCTCTGCAATAGTCCCTTGGAGGACCAAA 600
Db 541 TGCACTCTGGTGTCTGCTCATCTGTGTTGGCATCTCTGCAATAGTCCCTTGGAGGACCAAA 600
Qy 601 GTACAGGAAGACGTGCGATGATTAAGTGTCTTTCAGATTTCCAGATGATGATCTATCC 660
Db 601 GTACAGGAAGACGTGCGATGATTAAGTGTCTTTCAGATTTCCAGATGATGATCTATCC 660

RESULT 6
US-09-341-446B-5
; Sequence 5, Application US/09341446B
; Patent No. 6518480
; GENERAL INFORMATION:
; APPLICANT: Conklin, Bruce R.
; TITLE OF INVENTION: Selective Target Cell Activation By
; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated
; TITLE OF INVENTION: Superiorly By Synthetic Ligand
; FILE REFERENCE: UCAL-049CIP
; CURRENT APPLICATION NUMBER: US/09/341,446B
; CURRENT FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US97/05334
; PRIOR FILING DATE: 1997-03-25
; PRIOR APPLICATION NUMBER: US 08/622,348
; PRIOR FILING DATE: 1996-03-26
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1275
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: RASL OR1
US-09-341-446B-5

Query Match      86.6%; Score 999.4; DB 4; Length 1275;
Best Local Similarity 93.0%; Pred. No. 1.3e-246;
Matches 1061; Conservative 0; Mismatches 71; Indels 9; Gaps 1;

Qy 2 TGCACTCCCCGATCCAGATCTTCGGGGGAGCGCGGCCCTACTCGGCCCGGAGCGCCT 61
Db 113 TCAGACTCCCCGATCCAGATCTTCGGGGGAGCGCGGCCCTACTCGGCCCGGAGCGCCT 172
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QY 62 GCCTGCCCCCAACAGCAGCGCTGGTTTCCTCCGGCTGGGCGGAGCCCGACAGCAACGGCA 121
Db 173 GCCTGCCCCCAACAGCAGCGCTGGTTTCCTCCGGCTGGGCGGAGCCCGACAGCAACGGCA 232
QY 122 GCGCCGGCTCGAGAGAGCGCGCAGCTGGAGCCCGCGCACATCTCCCGCGGCATCCCGGTCA 181
Db 233 GCGCCGGCTCGAGAGAGCGCGCAGCTGGAGCCCGCGCACATCTCCCGCGGCATCCCGGTCA 292
QY 182 TCATCAGCGGCTCTACTCGTAGTGTCTGCTGGGCTTGGTGGCAACTCGCTGTCA 241
Db 293 TCATCAGCGGCTCTACTCGTAGTGTCTGCTGGGCTTGGTGGCAACTCGCTGTCA 352
QY 242 TGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAATTTACATATTTAAC 301
Db 353 TGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAATTTACATATTTAAC 412
QY 302 TGGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCTTTCAGAGTAGCGTCTACTTGA 361
Db 413 TGGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCTTTCAGAGTAGCGTCTACTTGA 472
QY 362 TGAATTCCTGGCCCTTTTGGGATGCTGTGCAAGATAGTAATTTCCATTGTACTACA 421
Db 473 TGAATTCCTGGCCCTTTTGGGATGCTGTGCAAGATAGTAATTTCCATTGTACTACA 532
QY 422 ACATGTTCCAGCAGCATCTTTCACCTTGACCATGATGAGCGTGGACCGCTACATTCGCGTGT 481
Db 533 ACATGTTCCAGCAGCATCTTTCACCTTGACCATGATGAGCGTGGACCGCTACATTCGCGTGT 592
QY 482 GCACCCCGTGAAGGCTTTGGCACTTCCGCACACCTTTGAAGCAAAAGATCATCAATATCT 541
Db 593 GCACCCCGTGAAGGCTTTGGCACTTCCGCACACCTTTGAAGCAAAAGATCATCAATATCT 652
QY 542 GCATCTGGCTGCTGTCATCTGTTGGCATCTCTGCAATAGTCCCTTGGAGGACCAAG 601
Db 653 GCATCTGGCTGCTGTCATCTGTTGGTATATCAGCATAGTCTTGGGGTGACCAAC 712
QY 602 TCAGGGAAGACGTCGATGTCAATGAGTGTCTTTCAGTGTCCAGATGATGACTACTCCT 661
Db 713 CCAGGATGGAGCAGTGATGATGACGCTCAGTTCCTCCAGCCC-----CAGCTGGT 763
QY 662 GGTGGGACCTCTTCATGAAGATCTGGGTCTTCACTTTGGCTTGTGATCCCTGTCTCA 721
Db 764 ACTGGGACACATGTGACCAAGATCTGGGTCTTCACTTTGGCTTGTGATCCCTGTCTCA 823
QY 722 TCATCATCTGCTCTACACCTCATGATCTCTGCTCTCAAGAGCTCCGCTCTCTTCTG 781
Db 824 TCATCATCTGCTCTACACCTCATGATCTCTGCTCTCAAGAGCTCCGCTCTCTTCTG 883
QY 782 GCTCCGAGAGAAAGATCGCAACCTCGTAGGATCACAGACTGGTCTCTGGTGGTGTG 841
Db 884 GCTCCGAGAGAAAGATCGCAACCTCGTAGGATCACAGACTGGTCTCTGGTGGTGTG 943
QY 842 CAGTCTTGTGCTGTGAGCTCCCATTCACATATTCATCTGTGGTGGAGGCTCTGGGA 901
Db 944 CAGTCTTGTGCTGTGAGCTCCCATTCACATATTCATCTGTGGTGGAGGCTCTGGGA 1003
QY 902 GCACCTCCACAGCAGCTGCTCTCCAGCTATTACTTCTGCTATGCTTAGGCTATA 961
Db 1004 GCACCTCCACAGCAGCTGCTCTCCAGCTATTACTTCTGCTATGCTTAGGCTATA 1063
QY 962 CCAACAGTAGCTGAATCCCATTTCTCTACGCTTTCTTGATGAAACTTCAAGCGGTGT 1021
Db 1064 CCAACAGTAGCTGAATCCCATTTCTCTACGCTTTCTTGATGAAACTTCAAGCGGTGT 1123
QY 1022 TCCGGGACTTCTGCTTTTCACTGAAGATGAGGATGGAGCGGAGAGCATAGCAGATGCC 1081
Db 1124 TCCGGGACTTCTGCTTTTCACTGAAGATGAGGATGGAGCGGAGAGCATAGCAGATGCC 1183
QY 1082 GAATACAGTTACAGTCTCTGCTTACTGAGGACATCCGATGGGATGAATAAACAGTAT 1141
Db 1184 GAATACAGTTACAGTCTCTGCTTACTGAGGACATCCGATGGGATGAATAAACAGTAG 1243
QY 1142 G 1142
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Db 1244 G 1244

#### RESULT 7

US-09-341-446B-7

; Sequence 7, Application US/09341446B

; Patent No. 6518480

; GENERAL INFORMATION:

; APPLICANT: Konklin, Bruce R.

; TITLE OF INVENTION: Selective Target Cell Activation By

; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated

; FILE OF INVENTION: Superiorly By Synthetic Ligand

; FILE REFERENCE: UCAL-049CIP

; CURRENT APPLICATION NUMBER: US/09/341,446B

; CURRENT FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US97/05334

; PRIOR FILING DATE: 1997-03-25

; PRIOR APPLICATION NUMBER: US 08/622,348

; PRIOR FILING DATE: 1996-03-26

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7

; LENGTH: 1275

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: RASL OR2

; US-09-341-446B-7

#### Query Match

Best Local Similarity 86.2%; Score 994.6; DB 4; Length 1275;

Matches 1058; Conservative 92.7%; Pred. No. 2.2e-245;

Mismatches 10; Indels 9; Gaps 1;

QY 2 TGAATCTCCCGATCCAGATCTTCCGCGGGAGCGCGGCGCTTACCTGCGCCCGAGCGCT 61

Db 113 TCGACTCCCGATCCAGATCTTCCGCGGGAGCGCGGCGCTTACCTGCGCCCGAGCGCT 172

QY 62 GCGTGCCTCCCAACAGCAGCGCTGTTTCCCGGCTGGGCGGAGCCCGACAGCAACGGCA 121

Db 173 GCGTGCCTCCCAACAGCAGCGCTGTTTCCCGGCTGGGCGGAGCCCGACAGCAACGGCA 232

QY 122 GCGCGGCTCGGAGGACGCGAGCTGGAGCCCGCGCACATCTCCCGGCGCATCCCGGTCA 181

Db 233 GCGCGGCTCGGAGGACGCGAGCTGGAGCCCGCGCACATCTCCCGGCGCATCCCGGTCA 292

QY 182 TCATCAGCGGCTCTACTCCGTAGTGTTCGTGCTGGGCTTGGTGGCAACTCGCTGTCA 241

Db 293 TCATCAGCGGCTCTACTCCGTAGTGTTCGTGCTGGGCTTGGTGGCAACTCGCTGTCA 352

QY 242 TGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAATTTACATATTTAAC 301

Db 353 TGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAATTTACATATTTAAC 412

QY 302 TGGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCTTTCAGAGTAGCGTCTACTTGA 361

Db 413 TGGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCTTTCAGAGTAGCGTCTACTTGA 472

QY 362 TGAATTCCTGGCCCTTTTGGGATGCTGTGCAAGATAGTAATTTCCATTGTACTACA 421

Db 473 TGAATTCCTGGCCCTTTTGGGATGCTGTGCAAGATAGTAATTTCCATTGTACTACA 532

QY 422 ACATGTTCCAGCAGCATCTTTCACCTTGACCATGATGAGCGTGGACCGCTACATTCGCGTGT 481

Db 533 ACATGTTCCAGCAGCATCTTTCACCTTGACCATGATGAGCGTGGACCGCTACATTCGCGTGT 592

QY 482 GCCACCCCGTGAAGGCTTTGGACTTCCGCACACCTTTGAAGGCAAAAGATCATCAATATCT 541

Db 593 GCCACCCCGTGAAGGCTTTGGACTTCCGCACACCTTTGAAGGCAAAAGATCATCAATATCT 652

QY 542 GCATCTGGCTGCTGCTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGACCAAG 601

Db 653 GCATCTGGCTGCTGCTCATCTGTTGGTATATCAGCGGATGCTCTTGGGTGACCAAC 712





Db 1144 ACCAACAGCAGCCTGAATCTGTTCTCTATGCTTCTTGATGAAATCTTCAAGCGGTCT 1203  
QY 1021 TTCCGGGACTTGTCTTTCACCTGAAGATGAGATGAGCGGCGAGAGCTAGCAGAGTC 1080  
Db 1204 TTTAGGGAATCTGCTTCCCTATTAAGATGCGAATGAGCGGCGAGAGCACCAGTAGAGTT 1263  
QY 1081 CGAAATACAGTTCAGGATCTGCTTACCTGAGGACATCGATGGGATGAATAACCCAGTA 1140  
Db 1264 AGAAACACAGTTCAGGATCTGCTTCCATGAGAGATGTGGAGGGATGAATAAGCCAGTA 1323  
QY 1141 TGAAGTCTGTGGA 1154  
Db 1324 TGAAGTCTGTGGA 1337

## RESULT 9

US-08-147-592A-1  
; Sequence 1, Application US/08147592A  
; Patent No. 6096513  
; GENERAL INFORMATION:  
; APPLICANT: Bell, Graeme I  
; APPLICANT: Reisine, Terry  
; APPLICANT: Yasuda, Kazuki  
; TITLE OF INVENTION: Opioid Receptor Genes,  
; TITLE OF INVENTION: Compositions and Methods  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States of America  
; ZIP: 72210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/147,592A  
; FILING DATE: 05-NOV-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/100,694  
; FILING DATE: 30-JUL-1993  
; CLASSIFICATION: 435  
; APPLICATION NUMBER: 08/066,296  
; FILING DATE: 20-MAY-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wilson, Mark B.  
; REGISTRATION NUMBER: 37,259  
; REFERENCE/DOCKET NUMBER: ARCD:105  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 474-7577  
; TELEX: N/A  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1410 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 186..1325  
US-08-147-592A-1

Query Match 79.1%; Score 912.4; DB 3; Length 1410;  
Best Local Similarity 86.9%; Pred. No. 3e-224;  
Matches 1003; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

QY 1 ATGGACTCCCGATCCAGATCTTCCGCGGGAGCCGGCCCTTACCTCGCCGCCCGAGCGCC 60  
Db 186 ATGGAGTCCCCATTCAGATCTTCCGAGAGATCCAGGCCCTTACCTGCTCTCCAGTGT 245  
QY 61 TGCCTGCCCCCAACAGCAGCGCTTGGTTTCCCGCTGGGCGAGCCCGCAGCAGCAACGGC 120  
Db 246 TGCCTTCTCCCAACAGCAGCTCTTGGTTCCCACTGGGCGAGAATCCGACAGTAATGCG 305  
QY 121 AGCGCGGCTCGGAGAGCGCGAGCTGGAGCCCGGCACATCTCCCGCCCATCCGGTTC 180  
Db 306 AGTGTGGGCTCAGAGGATCAGCAGCTGGAGTCCGCGCACATCTCTCCGCGCATCCCTGT 365  
QY 181 ATCATCAGCGGCTCTACTCCGCTAGTGTTCGTCGTGGGCTTGGTGGGCAATCTCGCTG 240  
Db 366 ATCATCAGCGCTCTACTCTGTGTATTTGGTGGGCTTAGTGGGCAATCTCTGTGTC 425  
QY 241 ATGTTGCTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTAAC 300  
Db 426 ATGTTTGTCTATCATCCGATACACGAAGATGAAGACCGCAACCAACATCTACATATTAAC 485  
QY 301 CTGGCTTTGGCAGATGCTTTAGTTACTACCAATGCTCCCTTTTCAGAGTACGCTACTTG 360  
Db 486 CTGGCTTTGGCAGATGCTTTGGTTACTACCATATGCCCCCTTTCAGAGTCTGTCTACTG 545  
QY 361 ATGAATTTCTGGCCCTTTTGGGATGTGTGTGCAAGATAGTAATTTCCATTGATTACTAC 420  
Db 546 ATGAATTTCTGGCCCTTTTGGAGATGTGTATGCAAGATTTGTCTATTTCCATTGACTACT 605  
QY 421 AACATGTTCCAGCATCTTCACTTGCATGATGAGGCTGGAGCCGCTACATTTGCCGTG 480  
Db 606 AACATGTTTACCAGCATATTTCACTTGCATGATGAGTGGAGCCGCTACATTTGCTGTG 665  
QY 481 TGCACCCCGTGAAGCTTTGGACTTCCGCACACCTTTGAAGGCAAGATCATCAATATC 540  
Db 666 TGCCACCCCTGTGAAGCTTTGGACTTCCGACACCTTTGAAGCAAGATCATCAATATC 725  
QY 541 TGCATCTGGCTGCTGTCTGTCATCTGTGTCATCTCTGCAATAGTCTTGGAGGCAACAAA 600  
Db 726 TGCATTTGGCTCTCTGGCATCATCTGTGTGTATATCAGCGATAGTCTTGGAGGCAACAAA 785  
QY 601 GTCAGGGAAGAGCTCGATGTCTATGAGTGTCTCTTGCAGTTCCTCAGATGATGACTACTCC 560  
Db 786 GTCAGGGAAGAGTGTGATGTCTATGAATGCTCTTGCAGTTCCTCAGATGATGAATATTC 845  
QY 661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCTATCTTGTGCTTGTGATCCTGTCTCTC 720  
Db 846 TGGTGGGATCTCTTCATGAAGATCTGTCCTTGTGCTTGTGCTTGTGATCCAGTCTCTC 905  
QY 721 ATCATCATCTGCTGTCTACACCTGATGATCTCGCTCTCAAGAGCGTCCGGTCTCTTTCT 780  
Db 906 ATCATCATTTGTCTGTCTACACCTGATGATCTCTGCGCTGAAGAGTGTCCGGCTCTGTCT 965  
QY 781 GGCTCCGAGAAAGATGCGAACCTGCTAGATACACAGACTGCTGCTGGTGGTGGTG 840  
Db 966 GGCTCCGAGAAAGAGCAGAAATCTCCGCCCATCACCAAGCTGGTGTGTGTAGTAGTT 1025  
QY 841 GCAGTCTTCTGCTGTCTGAGTCTCCATTCACATATTCATCTGCTGGTGGAGGCTCTGGGG 900  
Db 1026 GCAGTCTTCTATCTGTTGGACCCCATTCACATCTTTATCTGCTGGTGGAGGCTCTGGGA 1085  
QY 901 AGCACCTCCACAGACAGCTGCTCTCTCCAGTATTTACTTTCGANTTCCCTTAGGCTAT 960  
Db 1086 AGCACCTCCACAGACAGCTGCTCTCTCCAGTATTTACTTCTGATTTGCTTGGTGGTAT 1145  
QY 961 ACCACAGTAGCTGATCCCATCTCTACGCTTCTTGTATGAAACCTTCAAGCGGTGT 1020  
Db 1146 ACCACAGTAGCTGATCCCATCTCTATGCTTCTGATGCTTCTGATGAAACCTTCAAGCGGTGT 1205  
QY 1021 TTCCGGGACTTCTGCTTTCACCTGAAGATGAGATGAGCGGCGAGAGCTAGCAGAGTC 1080  
Db 1206 TTTAGGGAATCTGCTTCCCTATTAAGATGCGAATGAGCGGCGAGAGCACCAGTAGAGTT 1265  
QY 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAACCCAGTA 1140



Db 1266 AGAACACAGTTCAGGATCCTGCTTCATGAGAGATGGGAGGATGAATAAGCCAGTA 1325  
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Qy 1141 TGACTAGTCGTGGA 1154  
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Db 1326 TGACTAGTCGTGGA 1339  
|||||

## RESULT 10

US-08-292-694A-1  
; Sequence 1, Application US/08292694A  
; Patent No. 6319686  
; GENERAL INFORMATION:  
; APPLICANT: BELL, GRAEME  
; APPLICANT: REISINE, TERRY  
; APPLICANT: YASUDA, KAZUKI  
; TITLE OF INVENTION: OPIOID RECEPTORS: COMPOSITIONS AND METHODS  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P. O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/292,694A  
; FILING DATE: August 19, 1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/066,296  
; FILING DATE: 20 May 1993  
; CLASSIFICATION: 435  
; APPLICATION NUMBER: 08/100,694  
; FILING DATE: 30 July, 1993  
; CLASSIFICATION: 435  
; APPLICATION NUMBER: 08/147,592  
; FILING DATE: 5 No. 6319686ember 1993  
; CLASSIFICATION: 435  
; APPLICATION NUMBER: PCT/US94/05747  
; FILING DATE: 20 May 1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MARK B. WILSON  
; REGISTRATION NUMBER: 37,259  
; REFERENCE/DOCKET NUMBER: ARCD:140/WIM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (713) 789-2679  
; TELEX: 79-0924  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1410 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: genomic DNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 186..1325  
US-08-292-694A-1

Query Match 79.1%; Score 912.4; DB 3; Length 1410;  
Best Local Similarity 86.9%; Pred. No. 3e-224;  
Matches 1003; Conservative 0; Mismatches 151; Indels 0; Gaps 0;  
Qy 1 ATGCACTCCCGATCCAGATCTTCGGGGGAGCCGGCCCTACTCGGCCCGCCGAGGCC 60  
|||||

Db 186 ATGAGTCCCCCAATTCAGATCTTCCGAGGAGATCCAGGCCCTACTGCTCTCCAGTGCT 245  
Qy 61 TGCCTGCCCGCCCAACAGCAGCGCTGCTTTCCCGGCTGGCGCCGAGCCCGACAGCAACGGC 120  
Db 246 TGCCTTCTCCCAACAGCAGCGCTTGTGTTCCCACTGGGCGAGATCCGACAGTAATGCG 305  
Qy 121 AGCGCCGCTCGGAGGAGCGGAGCTGGAGCCCGGCACATCTCCCGGCGCATCCCGGTC 180  
Db 306 AGTGTGGGCTCAGAGGATCAGCAGCTGGAGTCCGCGCACATCTCTCCGGCCATCCCTGTT 365  
Qy 181 ATCATCACGGGCTACTCCGTAGTCTCGTCTGGGCTTGGTGGGCAACTCCGTGCTC 240  
Db 366 ATCATCACGGCTGCTACTCTGTGTATTTGTGTGGGCTTAGTGGGCAATCTCTGTGTC 425  
Qy 241 ATGTTCTGTATCATCCGATACACAAAGATGAAGACAGACCAACCAATTTACATATTAAC 300  
Db 426 ATGTTCTGTATCATCCGATACACAAAGATGAAGACCGCAACCAATTTACATATTAAC 485  
Qy 301 CTGCTTTGGCAGATGCTTTTAGTTACTACAAACATGCCCCTTTTACAGTACGGTCTACTG 360  
Db 486 CTGCTTTGGCAGATGCTTTTGGTTACTACCACTATGCCCTTTTACAGAGTGTCTACTTG 545  
Qy 361 ATGAATTCCTGGCCTTTTGGGATGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420  
Db 546 ATGAATTCCTGGCCTTTTGGAGATGCTATGCAAGATTTGCAATTCATTGACTACTAC 605  
Qy 421 AACATGTTTACCAGCATCTTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTG 480  
Db 606 AACATGTTTACCAGCATTTTCACTTGACCATGATGAGTGTGGACCGCTACATTGCTGTG 665  
Qy 481 TGCACCCCGTGAAAGGCTTTGGACTTCGGCACACCTTTGAAGGCAAAAGATCATCAATATC 540  
Db 666 TGCACCCCTGTGAAAGCTTTGGACTTCGGAACACCTTTGAAAGCAAAAGATCATCAACATC 725  
Qy 541 TGCATCTGGCTGCTGCTGCTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGCAACAA 600  
Db 726 TGCATTTGGCTTCTTGGCATCATCTGTTGGTATATCAGCGATAGTCTTGGAGGCAACAA 785  
Qy 601 GTCAGGGAAGACGTGCGATGTCTTGAAGTGTCTTTCAGTTCCTTCCAGATTCAGTACTTCC 660  
Db 786 GTCAGGGAAGATGTGGATGTCTTGAATGTCTTTCAGTTCCTTCCAGTTCAGTATATTC 845  
Qy 661 TGTGGGACCTTCTTATGAAGATCTGGCTTTTCACTTTTGGCTTTCGTGATCCCTGCTC 720  
Db 846 TGTGGGATCTCTTATGAAGATCTGTGTCTTTCGCTTTTGTGATCCAGTCTC 905  
Qy 721 ATCATCATCTGCTACACCTGTGATGATCTGGGCTCTCAAGCGTCCGGCTCTTCT 780  
Db 906 ATCATCATTTGCTGTACACCTGTGATGATCTCGGCTGGAAGAGTGTCCGGCTCTTCT 965  
Qy 781 GGCTCCCGAGAGAAAGATGCAACCTGCTAGGATCACCAGACTGGTCTCGTGGTGGTG 840  
Db 966 GGCTCCCGAGAGAAAGACCGAATCTCCGCGCATCACAGCTGGTGTGGTAGTGT 1025  
Qy 841 GCAGTCTTCTGCTGTCTGGACTCCCATTCACATATTCATTCCTGGTGGAGGCTCTGGGG 900  
Db 1026 GCAGTCTTCTATCTCTTGGACCCCATTCACATCTTTTATCTGTTGGAGGCTCTGGGA 1085  
Qy 901 AGCACCTCCACAGCAGCTGCTCTCCAGCTATTACTTCTGCATTCGCTTAGGCTAT 960  
Db 1086 AGCACCTCCACAGCAGCTGCTCTCCAGCTATTATTCTGTATTTGCTTGGGTTAT 1145  
Qy 961 ACCAACAGTAGTCCGTAATCCATTTCTAGCCCTTTCTTGTATGAAATCTTCAAGCGGTG 1020  
Db 1146 ACCAACAGAGCTGTAATCTGTTCTATGCTTCTGATGAAATCTTCAAGCGGTG 1205  
Qy 1021 TTCGGGACTTCTGCTTTTCCATCAAGATGAGGATGGAGCGGCGAGACCTTAGCAGATC 1080  
Db 1206 TTTAGGAGACTTCTGCTTCCCTATTAAGATGCAATGGAGCGCCAGAGACCAATAGAGTT 1265  
Qy 1081 CGAAATACAGTTACAGGATCTGCTTACTCAGGAGACATCGATGGGATGAATAAACCCAGTA 1140  
Db 1266 AGAAACACAGTTTCCAGGATCTGCTTCCATGAGAGATGTGGAGGGATGAATAAACCCAGTA 1325

QY 1141 TGACTAGTCGTGGA 1154  
 Db 1326 TGACTAGTCGTGGA 1339

RESULT 11  
 US-08-147-592A-11  
 ; Sequence 11, Application US/08147592A  
 ; Patent No. 6096513  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bell, Graeme I  
 ; APPLICANT: Reisine, Terry  
 ; APPLICANT: Yasuda, Kazuki  
 ; TITLE OF INVENTION: Opioid Receptor Genes,  
 ; TITLE OF INVENTION: Compositions and Methods  
 ; NUMBER OF SEQUENCES: 43  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Arnold, White & Durkee  
 ; STREET: P.O. Box 4433  
 ; CITY: Houston  
 ; STATE: Texas  
 ; COUNTRY: United States of America  
 ; ZIP: 77210  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/147,592A  
 ; FILING DATE: 05-NOV-1993  
 ; CLASSIFICATION: 435  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/100,694  
 ; FILING DATE: 30-JUL-1993  
 ; CLASSIFICATION: 435  
 ; APPLICATION NUMBER: 08/066,296  
 ; FILING DATE: 20-MAY-1993  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Wilson, Mark B.  
 ; REGISTRATION NUMBER: 37,259  
 ; REFERENCE/DOCKET NUMBER: ARCD:105  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (512) 418-3000  
 ; TELEFAX: (512) 474-7577  
 ; TELEX: N/A  
 ; INFORMATION FOR SEQ ID NO: 11:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1000 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA  
 ; FEATURE:  
 ; NAME/KEY: N  
 ; LOCATION: 607-608, 642-643, 896, 906  
 ; IDENTIFICATION METHOD: N = A, C, G or T  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 102..986  
 ; FEATURE:  
 ; NAME/KEY: Xaa  
 ; LOCATION: 169, 181, 265, 269  
 ; IDENTIFICATION METHOD: Xaa = unknown  
 US-08-147-592A-11

Query Match 75.4%; Score 869.6; DB 3; Length 1000;  
 Best Local Similarity 97.5%; Pred. No. 2.5e-213;  
 Matches 891; Conservative 0; Mismatches 20; Indels 3; Gaps 1;  
 QY 244 TTCTGTATCCGATACACAAAGATGAAGACGACCAACCAATTTACATATTTAACTG 303

Db 87 TTCTTTTCTTTTAGATACACAAAGATGAAGACGACCAACCAATTTACATATTTAACTG 146  
 QY 304 GCTTTGGCAGATGCTTTAGTTACTACCAACCATGCGCTTTACAGATACGCTTACTTTGATG 363  
 Db 147 GCTTTGGCAGATGCTTTAGTTACTACCAACCATGCGCTTTACAGATACGCTTACTTTGATG 206  
 QY 364 AATTCTGCGCTTTTGGGGATGCTGTGCAAGATAGTAATTTCCATTGATTACTACCAAC 423  
 Db 207 AATTCTGCGCTTTTGGGGATGCTGTGCAAGATAGTAATTTCCATTGATTACTACCAAC 266  
 QY 424 ATGTTACCAAGCATCTTTCACCTTGACCATGATGAGCGTGACCGCTTACATTTGCCGTGTG 483  
 Db 267 ATGTTACCAAGCATCTTTCACCTTGACCATGATGAGCGTGACCGCTTACATTTGCCGTGTG 326  
 QY 484 CACCCCGTGAAGGCTTTGGGACTTTCGCGCACACCGTTGAAGCGAAAGATCATCAATATCTGC 543  
 Db 327 CACCCCGTGAAGGCTTTGGGACTTTCGCGCACACCGTTGAAGCGAAAGATCATCAATATCTGC 386  
 QY 544 ATCTGCTGCTGTCGTGTCATCTGTGGCATCTCTGCAATAGTCTCTTGGAGGACCAAGATC 603  
 Db 387 ATCTGCTGCTGTCGTGTCATCTGTGGCATCTCTGCAATAGTCTCTTGGAGGACCAAGATC 446  
 QY 604 AGGGAAGACGTCGATGTCTATTGAGTGCTCTTTCAGAGTTCCTCAGATGATGACTACTCTCTG 663  
 Db 447 AGGGAAGGTCGATGTCTATTGAGTGCTCTTTCAGAGTTCCTCAGATGATGACTACTCTCTG 506  
 QY 664 TGGGACCTCTTCATGAAGATCTGGCTTCTTCATCTTTCGCTTTCGATGATCCTGCTCTCATC 723  
 Db 507 TGGGACCTCTTCATGAAGATCTGGCTTCTTCATCTTTCGCTTTCGATGATCCTGCTCTCATC 566  
 QY 724 ATCATGCTGCTGTCATACCCCTGATGATCTCTGCTCTCAAGAGCGTCCGGCTCTCTTCTGCG 783  
 Db 567 ATCATGCTGCTGTCATACCCCTGATGATCTCTGCTCTCAAGAGCGTCCGGCTCTCTTCTGCG 626  
 QY 784 TCCCGAGAGAAAGATGCGAACCTGCGTAGGATCACCAGATCTGCTCTGCTGCTGCTGCTGCGA 843  
 Db 627 TCCCGAGAGAAAGATGCGAACCTGCGTAGGATCACCAGATCTGCTCTGCTGCTGCTGCTGCGA 686  
 QY 844 GTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 903  
 Db 687 GTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 746  
 QY 904 ACCTCCACAGACAGCTGCTGCTCTCCAGCTATTACTTCTGATTCCTTACGCTTATACCTAC 963  
 Db 747 ACCTCCACAGACAGCTGCTGCTCTCCAGCTATTACTTCTGATTCCTTACGCTTATACCTAC 806  
 QY 964 AACAGTAGCTGAATCCCATTTCTACGCTTTCTTTCGATGAAACTTCAAGCGGTGTTTC 1023  
 Db 807 AACAGTAGCTGAATCCCATTTCTACGCTTTCTTTCGATGAAACTTCAAGCGGTGTTTC 866  
 QY 1024 CGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGGCGGACGACGATGAGGATGAGGATGAG 1083  
 Db 867 CGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGGCGGACGACGATGAGGATGAGGATGAG 926  
 QY 1084 AATACAGTTTCAGGATCTCTGCTTACCTGAGGACATCGATGG--GATGAATAAACCACTA 1140  
 Db 927 AATACAGTTTCAGGATCTCTGCTTACCTGAGGATGAGGATGAGGATGAGGATGAGGATGAG 986  
 QY 1141 TGACTAGTCGTGGA 1154  
 Db 987 TGACTAGTCGTGGA 1000

RESULT 12  
 US-08-292-694A-11  
 ; Sequence 11, Application US/08292694A  
 ; Patent No. 6319686  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bell, Graeme  
 ; APPLICANT: Reisine, Terry  
 ; APPLICANT: YASUDA, KAZUKI  
 ; TITLE OF INVENTION: OPIOID RECEPTORS: COMPOSITIONS AND METHODS

NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P. O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
SOFTWARE: Patent In Release #1.0, Version #1.25

Qy	424	ATGTTCA	CAGCA	TCTTCA	CTTCA	CGATCA	TGATG	AGCGT	TGGA	CGCTAC	ATTG	CCGTGT	GC	483
Db	267	ATGTTCA	CACGAC	TCTTCA	CTTCA	CGATCA	TGATG	AGCGT	TGGA	CGCTAC	ATTG	CCGTGT	GC	326
Qy	484	CACCCGT	GAAGCT	TTTGA	CTTCC	GCAC	ACCCTT	GAAGCA	AAAGAT	CATCA	ATAAT	CTCTG	C	543
Db	327	CACCCGT	GAAGCT	TTTGA	CTTCC	GCAC	ACCCTT	GAAGCA	AAAGAT	CATCA	ATAAT	CTCTG	C	386
Qy	544	ATCTGG	CTGCTG	TCATCT	GTGTGG	CATCT	CTGCA	ATATG	CTCTTGG	AGGCAC	CAAAAG	TC	603	
Db	387	ATCTGG	CTGCTG	TCATCT	GTGTGG	CATCT	CTGCA	ATATG	CTCTTGG	AGGCAC	CAAAAG	TC	446	
Qy	604	AGGGA	AGCGT	CGATG	TCATTG	AGTG	CTCTT	GCAGT	TCCG	AGATG	ATGACT	CTCTG	663	
Db	447	AGGGA	AGGTG	TCGATG	TCATTG	AGTG	CTCTT	GCAGT	TCCG	AGATG	ATGACT	CTCTG	506	
Qy	664	TGGG	ACCTT	CATGA	AGATCT	CGCGT	CTTCA	CTTTT	GCCTT	CGTGAT	CCCTG	TCCTCAT	723	
Db	507	TGGG	ACCTT	CATGA	AGATCT	CGCGT	CTTCA	CTTTT	GCCTT	CGTGAT	CCCTG	TCCTCAT	566	
Qy	724	ATCAT	CGTCTG	CTAC	ACCCTG	ATGAT	CTT	CGCTCT	CAAGA	CGCT	CCGGT	CTCTTT	783	
Db	567	ATCAT	CGTCTG	CTAC	ACCCTG	ATGAT	CTT	CGCTCT	CAAGA	CGCT	CCGGT	CTCTTT	626	
Qy	784	TCCCG	GAGAA	AGATCG	CAAC	CTGCGT	AGATCA	CCAGACT	GGTCT	CGTG	TGTTGG	TGGCA	843	
Db	627	TCCCG	GAGAA	AGATNN	CAAC	CTGCGT	AGATCA	CCAGACT	GGTCT	CGTG	TGTTGG	TGGCA	686	
Qy	844	GTCTT	CGTCTG	CTGCTG	CAATCC	CAATAT	TTCAT	CCTCGT	GGAGCT	CTGGG	GAGC		903	
Db	687	GTCTT	CGTCTG	CTGCTG	CAATCC	CAATAT	TTCAT	CCTCGT	GGAGCT	CTGGG	GAGC		746	
Qy	904	ACCTT	CCAC	GACAC	AGCTG	CTCTCT	CCAGCTAT	TACTT	CTGCA	ATTGCC	TTAG	GCATAT	963	
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Qy	964	AA	CAGTAG	CTGAA	TCCCAT	CTCTA	AGCGCTTT	CTTGT	TGAG	AAAA	CTTCA	AGCGGT	1023	
Db	807	AA	CAGTAG	CTGAA	TCCCAT	CTCTA	AGCGCTTT	CTTGT	TGAG	AAAA	CTTCA	AGCGGT	866	
Qy	1024	CGGGA	CTTCTG	CTTTT	CCACTG	GAAGAT	GAGAT	TGGAG	CGCG	CAGAC	CACTAG	CAGAT	1083	
Db	867	CGGGA	CTTCTG	CTTTT	CCACTG	GAAGAT	GAGAT	TGGAG	CGCG	CAGAC	CACTAG	CAGAT	926	
Qy	1084	AATAC	AGTT	CAGGAT	CCTGCT	TACCT	GAGG	GACAT	CGAT	TGG---	GAT	GAATAA	1140	
Db	927	AATAC	AGTT	CAGGAT	CCTGCT	TACCT	GAGG	GACAT	CGAT	TGG---	GAT	GAATAA	986	
Qy	1141	TG	ACTAG	TCGT	GGA	1154								
Db	987	TG	ACTAG	TCGT	GGA	1000								

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RESULT 13
US-08-430-286A-1
; Sequence 1, Application US/08430286A
; Patent No. 6225080
; GENERAL INFORMATION:
; APPLICANT: Uhl, George R.
; APPLICANT: Epler, C. Mark
; APPLICANT: Wang, Jai-Bel
; TITLE OF INVENTION: Mu-Subtype Opioid Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: US
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/430,286A
/ FILING DATE: 28-APR-1995
/ CLASSIFICATION: 536
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Robinson, Joseph R.
/ REGISTRATION NUMBER: 33,448
/ REFERENCE/DOCKET NUMBER: 0646/1A843-US5
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 212-527-7700
/ TELEFAX: 212-753-6237
/ TELEX: 236687
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2135 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA to mRNA
/ ORIGINAL SOURCE:
/ ORGANISM: Rattus rattus
/ IMMEDIATE SOURCE:
/ CLONE: mu receptor cDNA
/ US-08-430-286A-1

Query Match 39.0%; Score 449.6; DB 3; Length 2135;
Best Local Similarity 67.1%; Pred. No. 2.4e-105;
Matches 670; Conservative 0; Mismatches 319; Indels 9; Gaps 2;

QY 110 ACAGCAACGCGCAGCGCGCTCGAGAGCGCGAGCTGGAGCGCGGCACATCTCCCGG 169
DB 167 ACCGCAACGCGGCTGGCGGAACGACGAGCTGTGCGCTCAGACCGCGACCTTCCATGG 226
QY 170 CCATCCCGGTCTATCATCAGCGCGGTCTACTCCGTAGTGTTCGTCGTGGGCTTGGTGGCA 229
DB 227 TCAGAGCATACCATCATGCGCCCTCTACTCTATCGTGTGTAGTGGGCTCTTCGGAA 286
QY 230 ACTCGGTGTGTCATGTCGTCATCCGATACACAAAGATGAAGACAGACCAACATTT 289
DB 287 ACTTCTGTGTGTCATGTATGTATGAATGTAAGATACACCAAAATGAAGCTGCCAACATCT 346
QY 290 ACATATTAACTGCTGTTGGAGAGCTTTAGTACTCAACCATGCGCCCTTTCAGAGTA 349
DB 347 ACATTTCACTGCTGCTGGAGAGCGCTTACGACCATGCTACTGCGCTTTCAGAGTG 406
QY 350 CGGTCTACTTGATGAATTCCTGGCCCTTTTGGGGATGTGCTGTGCAAGATAGTAATTCCA 409
DB 407 TCAACTACCTGATGGGAACATGSCCTTCGGAACCATCTCTGCAAGATCGTGATCTCAA 466
QY 410 TTGATTACTACAACATGTTCCAGCATCTTCACTTGACCATGATGAGGTGGACCGCT 469
DB 467 TAGATTACTACAACATGTTCCAGCATATTTCACTCTGTCACCATGAGGTGGACCGCT 526
QY 470 ACATTCGCTGTCGCAACCGCTTGGAGCTTTGGACTTCGCAACCATCTTCAAGGCAAGA 529
DB 527 ACATTCGCTGTCGCAACCGCTTGGAGCTTTGGACTTCGCAACCATCTTCAAGGCAAGA 586
QY 530 TCATCAATATCTGCACTGCTGCTGTCGTCATCTGTGTCATCTCTGCAATAGTCTCTTG 589
DB 587 TCGTCAACGCTGCAACTGGATCTCTCTTCTGCAATGCTGCTGCTGCTGCTGCTGCTGCTG 646
QY 590 GAGGCAACAAAGTCAGGGAAGAGCTGATGTCATTTGAGTGTCTCTTGGAGTCTCCAGATG 649
DB 647 CAACCAACAAATACAGGCGGGGTC-----CATAGATTGCACCTTCTCCACC 700
QY 650 ATGACTACTCTCTGCTGGAGCTCTTCATGAAGATCTGCGTCTTCTGCTGCTGCTGCTG 709
DB 701 CAACCTGCTGCTGGAGAACTGCTC-----AAATCTGCTGCTTCTGCTGCTGCTGCTG 757
QY 710 TCCCTGTCTCTCATCATCATCTGCTGCTGTACACCTGATGATCTCTGCTGCTCAAGAGCTGC 769
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DB 758 TGCCGCTCTCATCATCATCTGCTGTGTGTACGGCTGATGATCTTACGACTCAAGAGCGTTC 817
QY 770 GGCTCTCTTCTGGCTCCGAGAGAAAGATCGCAACTGGTAGGATCACCAGACTGGTCC 829
DB 818 GCATGCTATCGGGCTCCAAAGAAAGGACAGGAATCTGCGCAGGATCACCCGGATGGTGC 877
QY 830 TGGTGTGTGTCAGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 889
DB 878 TGGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 937
QY 890 AGGCTCTGCGGAGCACCTCCACAGACAGCTGCTCTCTTCCAGCTTATTAATCTTCTGCTG 949
DB 938 AAGCGCTGATCAGGATTCAGAAACACATTTCCAGACCGTCTTCTGCGCACTTCTGCTGCTG 997
QY 950 CTTAGGCTATACCAACAGTAGCTGATCCCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1009
DB 998 CTTTGGGTTACACGAAACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1057
QY 1010 TCAAGCGGTGTTTCCGGGACTTCTGCTTCTTCCACTGAAGATGAGGATGGAGCGGAGAGCA 1069
DB 1058 TCAGCGATGCTTTCAGAGATTTCTGATCCCAACCTGCTCCAGATCGAGACGAGCAAACT 1117
QY 1070 CTAGCAGAGTCGAAATACAGTTTCAGGATCTGCTTAC 1107
DB 1118 CCACTCGAGTCGTCAGAACACTAGGGAACATCCCTCC 1155

RESULT 14
US-08-889-108-1
; Sequence 1, Application US/08889108
; Patent No. 6103492
; GENERAL INFORMATION:
; APPLICANT: Yu, Lei
; TITLE OF INVENTION: Mu Opioid Receptors: Compositions and Methods
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESS: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/889,108
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/305,518
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: INDA005\WIM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1618 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (cdna)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 214..1410
; US-08-889-108-1
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Query Match      38.8%; Score 448; DB 3; Length 1618;
Best Local Similarity 67.0%; Pred. No. 5.4e-105;
Matches 669; Conservative 0; Mismatches 320; Indels 9; Gaps 2;

Qy 110 ACAGCAACGGCAGCGCGCTCGAGGAGCGGAGCTGGAGCGCGGCACATCTCCCGG 169
Db 350 ACCGACCGGCTTGGCGGAGACGACGCTGTGCGCTCAGACCGGAGCCCTTCCATGG 409
Qy 170 CCATCCCGGTCAATCATCAGCGCGGTCTACTCCGTAGTGTTCGTGCGGCTTGGGCA 229
Db 410 TCACAGCCATTACCATCATCGCCCTTACTCTATCTGTGTGTAGTGGCTCTTCGAA 469
Qy 230 ACTCGCTGGTCATGTTTCGTGATCATCGGATACACAAAGATGAAGACAGCAACCAATTT 289
Db 470 ACTTCTCGTCAATCATCGCCCTTACTCTATCTGTGTGTAGTGGCTCTTCGAA 469
Qy 290 ACATATTTAACTGGCTTGGCAGATGCTTTAGTTACTACACCATGCGCTTTCAGAGTA 349
Db 530 ACATTTTCAACCTTGTCTGGCAGACGCTTAGCAGCAGTACACTGCGCTTTCAGAGTG 589
Qy 350 CGGTCTACTTGATGAATTCCTGGCGCTTTCGGGATGTCTGTGCAAGATAGTAATTTCCA 409
Db 590 TCACTACTGATGGGAACATGGCCCTTCGGAACCATCTCTGCAAGATCGTATCTCAA 649
Qy 410 TTGATTACTACAACATGTTTACCAGCATCTTTCACCTTGACCATGATGAGCGTGACCGCT 469
Db 650 TAGATTACTACAACATGTTTACCAGCATATTCACCTCTGCACCATGAGCGTGACCGCT 709
Qy 470 ACATTTGGCTGTGCCACCGCTTGAAGGCTTTGGACTTCGGACACCCCTTGAAGGCAAGA 529
Db 710 ACATTTGTGTCTGCCACCGCTTGAAGGCTTGGATTTTCCGTACCCCGGAAATGCCAAA 769
Qy 530 TCATCAATATCTGATCTGGCTGTCTGCTCATCTGTTGGCATCTCTGCAATAGTTCCTTG 589
Db 770 TCGTCAAGTCTGCACTGGATCTCTCTTCTGCGATCGCTGCTGCTGTAATGTTCAAG 829
Qy 590 GAGGACCAAAAGTCAGGAAGACGTCGATGTCATTTAGTGTCTCTTGCAGTTCCAGATG 649
Db 830 CAACCAACAAATACAGGAGGCGTC-----CATAGATTGCACCTCAGCTTCTCCACC 883
Qy 650 ATGACTACTCTGGTGGGACCTCTTCATGAAGATCTGGCTTCTCATCTTTCCTTGTGA 709
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Qy 710 TCCGTCTCTCATCATCATCTGCTGTCTACACCTGTGATGATCTCGCTCTCAAGAGCGTCC 769
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Qy 770 GGCTCCTTTCTGGCTCCGAGAGAAAGATCGCAACCTGCGTAGGATCACCAGACTGGTCC 829
Db 1001 GCATGCTATCGGCTCCAAAGAAAGGACAGGAATCTGGCAGGATCACCAGGATGGTGC 1060
Qy 830 TGGTGGTGGGAGTCTTCTGCTGTCTGCTGAGCTCCGATTCATATTCATCTCTGGTGG 889
Db 1061 TGGTGGTGGTGGTGTATTTATCTGCTGTCTGAGACCCCATCCATCATCTACGTCATCA 1120
Qy 890 AGGCTCTGGGAGACCTCCACAGCAGCTGTCTCTCCAGTATTACTTCTGCAATG 949
Db 1121 AAGCGCTGATCAGATTCAGAAACCAATTCAGACCGTTTCTTGGACATCTTGCATTTG 1180
Qy 950 CTTTAGGCTATACCAACAGTAGTCCGATTCATCTTCTAGCGCTTCTTCTGATGAAACT 1009
Db 1181 CTTTGGGTTACAGACAGCTGCTGATTCAGTCTTCTTACGCTTCTTCTGATGAAACT 1240
Qy 1010 TCAAGCGGTGTTTCCGGGACTTCTGCTTTCATCTGAAGATGAGGATGAGGCGGAGCA 1069
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Qy 1070 CTAGCAGAGTCCGAAATACAGTTCCAGGATCTGCTTAC 1107
Db 1301 CCACTCGAGTCCGTGAGAACACTAGGGAACATCCCTCC 1338
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RESULT 15
US-08-889-108-3
; Sequence 3, Application US/08889108
; Patent No. 6103492
; GENERAL INFORMATION:
; APPLICANT: Yu, Lei
; TITLE OF INVENTION: Mu Opioid Receptors: Compositions and Methods
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/889,108
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/305,518
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: INDA005\WIM
; TELEPHONE: 512-418-3000
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1618 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (cdna)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 339..1235
; US-08-889-108-3
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Query Match      38.8%; Score 448; DB 3; Length 1618;
Best Local Similarity 67.0%; Pred. No. 5.4e-105;
Matches 669; Conservative 0; Mismatches 320; Indels 9; Gaps 2;

Qy 110 ACAGCAACGGCAGCGCGCTCGAGGAGCGGAGCTGGAGCGCGGCACATCTCCCGG 169
Db 350 ACCGACCGGCTTGGCGGAGACGACGCTGTGCGCTCAGACCGGAGCCCTTCCATGG 409
Qy 170 CCATCCCGGTCAATCATCAGCGCGGTCTACTCCGTAGTGTTCGTGCGGCTTGGGCA 229
Db 410 TCACAGCCATTACCATCATCGCCCTTACTCTATCTGTGTGTAGTGGCTCTTCGAA 469
Qy 230 ACTCGCTGGTCATGTTTCGTGATCATCGGATACACAAAGATGAAGACAGCAACCAATTT 289
Db 470 ACTTCTCGTCAATCATCGCCCTTACTCTATCTGTGTGTAGTGGCTCTTCGAA 529
Qy 290 ACATATTTAACTGGCTTGGCAGATGCTTTAGTTACTACACCATGCGCTTTCAGAGTA 349
Db 530 ACATTTTCAACCTTGTCTGGCAGACGCTTAGCAGCAGTACACTGCGCTTTCAGAGTG 589
Qy 350 CGGTCTACTTGATGAATTCCTGGCGCTTTCGGGATGTCTGTGCAAGATAGTAATTTCCA 409
Db 590 TCACTACTGATGGGAACATGGCCCTTCGGAACCATCTCTGCAAGATCGTATCTCAA 649
Qy 410 TTGATTACTACAACATGTTTACCAGCATCTTTCACCTTGACCATGATGAGCGTGACCGCT 469
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Db 650 TAGATTACTACAAATGTTTACACAGATATTACCCCTCTGCACCATGACGCTGGACCGCT 709  
 Qy 470 ACATTGCCGTGTGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCCTTTGAAGGCAAAAGA 529  
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 Qy 530 TCATCAATATCTGCATCTGGTCTGTCTCATCTGTGGCATCTCTGCAATAGTCCCTTG 589  
 Db 770 TCGTCAACGCTGTCAATCGATCCTCTCTCTGCCCACGCTGTGCTGTAAATGTTTCATGG 829  
 Qy 590 GAGGCACCAAGTCAGGGAAGCGTGTGATGATGAGTCTCTTGCAGATTTCCAGATG 649  
 Db 830 CAACCAAAATACAGCGGGGTC-----CATAGATTGCACCCCTCACGTTCTCCACCC 883  
 Qy 650 ATGACTACTCCTGGTGGGACCTCTTCATGAAGATCTGGCTCTTCATCTTTGGCTTCGTGA 709  
 Db 884 CAACCTGGTACTGGGAGAACCTGCTC---AAATCTGTCTTTATCTTCGCTTTTCATCA 940  
 Qy 710 TCCCTGCTCATCATCATCTGTCTGTACACCTGTATGATCTGTGCTCTCAAGAGCGTCC 769  
 Db 941 TGCCGATCTCTCATCATCTGTGTATCGGCTGTATGATCTTACGACTCAAGAGCGTTC 1000  
 Qy 770 GGCTCCTTTCTGGCTCCCGAGAGAAAGATCGCAACCTGGGTAGGATCACAGACTGTCTCC 829  
 Db 1001 GCATGCTATCGGCTCCAAAGAAAGAGACAGGAATCTGGCAGGATCACCCGGATGTGC 1060  
 Qy 830 TGGTGGTGGGAGCTTTCGTCTGTGTGGACTCCCATTCACATATTCACTCTGGTGG 889  
 Db 1061 TGGTGGTGGTGGTGTATTATCTGTGTGGACCCCGCATCCACATCTACGTCATCATCA 1120  
 Qy 890 AGGCTCTGGGGAGCACCTCCACAGACAGCTGCTCTCTCCAGCTATTACTTCTGCATTG 949  
 Db 1121 AAGCGTGATCAGATTCAGAAACACATTCAGACCGTTTCTGGCACTTCTGCATTG 1180  
 Qy 950 CCTTAGGCTATACCAAGTAGCTGAATCCCATTTCTACGCTTTCTTGATGAAACT 1009  
 Db 1181 CTTTGGTTACAGACAGCTGCTGAATCCAGTCTTTACGCTTCTCTGGATGAAACT 1240  
 Qy 1010 TCAAGCGGTGTTCCGGGACTTCTGCTTCCACTGAAGATGAGGATGGAGCGGCAGCA 1069  
 Db 1241 TCAAGCGATGCTTCAGAGAGTTCTGCATCCCAACCTCGTCCAGCATCGAACAGCAAAACT 1300  
 Qy 1070 CTAGCAGATCCGAATACAGTTTCAAGTCTGCTTAC 1107  
 Db 1301 CCCTCGATCCGTCAGAACACTAGGGAACATCCCTCC 1338

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 Job time : 218 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model  
Run on: April 6, 2005, 12:28:42 ; Search time 766.333 Seconds  
(without alignments)  
9125.590 Million cell updates/sec

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Perfect score: 1154  
Sequence: 1 atggactcccgatccagat.....ccagatgactagctgtgga 1154

Scoring table: IDENTITY\_NUC  
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Searched: 5615251 seqs, 3030001701 residues  
Total number of hits satisfying chosen parameters: 11230502

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Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	1152.4	99.9	1602	19	US-10-278-698-559
5	1150.8	99.7	1154	11	US-09-904-584-2
6	1150.8	99.7	1154	11	US-09-904-584-4
7	1150.8	99.7	1154	11	US-09-904-584-5
8	1150.8	99.7	1154	11	US-09-904-584-6
9	1150.8	99.7	1154	11	US-09-904-584-7
10	1144.4	99.2	1182	15	US-10-225-567A-147
11	1144.4	99.2	1182	15	US-10-345-680-19

12	1144.4	99.2	1182	17	US-10-305-720-1417	Sequence 1417, Ap
13	1144.4	99.2	1182	18	US-10-283-975A-80	Sequence 80, Appl
14	1141.4	98.9	1143	16	US-10-318-661-1	Sequence 1, Appli
15	1136.2	98.5	1284	16	US-10-318-661-3	Sequence 3, Appli
16	1133.4	98.2	1143	15	US-10-345-680-21	Sequence 21, Appl
17	1130.2	97.9	1143	10	US-09-826-509-542	Sequence 542, App
18	1130.2	97.9	1143	19	US-10-925-095-542	Sequence 542, App
19	999.4	86.6	1275	16	US-10-318-661-5	Sequence 5, Appli
20	994.6	86.2	1275	16	US-10-318-661-7	Sequence 7, Appli
21	979.4	84.9	1875	16	US-10-318-661-13	Sequence 13, Appli
22	963.4	83.5	1875	16	US-10-318-661-15	Sequence 15, Appli
23	912.4	79.1	1408	9	US-09-214-904-5	Sequence 5, Appli
24	877.8	76.1	1911	16	US-10-318-661-17	Sequence 17, Appl
C 25	469	40.6	585	13	US-10-027-632-188121	Sequence 188121,
C 26	469	40.6	585	13	US-10-027-632-188122	Sequence 188122,
C 27	469	40.6	585	17	US-10-027-632-188121	Sequence 188121,
C 28	469	40.6	585	17	US-10-027-632-188122	Sequence 188122,
29	448	38.8	1618	10	US-09-841-720-1	Sequence 1, Appli
30	448	38.8	1618	10	US-09-841-720-3	Sequence 3, Appli
31	437.8	37.9	1464	14	US-10-185-083-25	Sequence 25, Appl
32	436.4	37.8	1239	14	US-10-080-917-10	Sequence 10, Appl
33	436.4	37.8	1245	14	US-10-080-917-8	Sequence 8, Appli
34	436.4	37.8	1388	14	US-10-185-083-26	Sequence 26, Appl
35	436.4	37.8	1431	14	US-10-080-917-6	Sequence 6, Appli
36	436.4	37.8	2149	14	US-10-080-917-12	Sequence 12, Appl
37	436.4	37.8	2162	11	US-09-883-839-1	Sequence 1, Appli
38	436.4	37.8	2162	11	US-09-883-839-3	Sequence 3, Appli
39	436.4	37.8	2162	11	US-09-883-839-5	Sequence 5, Appli
40	436.4	37.8	2162	15	US-10-225-567A-185	Sequence 185, App
41	436.4	37.8	2162	17	US-10-305-720-1379	Sequence 1379, Ap
42	436.4	37.8	2279	19	US-10-477-714-33	Sequence 33, Appl
43	434.8	37.7	1176	10	US-09-935-061-11	Sequence 11, Appl
44	434.8	37.7	1176	18	US-10-692-071-11	Sequence 11, Appl
45	434.8	37.7	1473	14	US-10-080-917-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1  
US-09-904-584-3  
; Sequence 3, Application US/09904584  
; Publication No. US20040097704A1  
; GENERAL INFORMATION:  
; APPLICANT: Kreek, Mary Jeanne  
; APPLICANT: Yuforov, Vadim  
; APPLICANT: LaForge, Karl Steven  
; TITLE OF INVENTION: Alleles of the Human Kappa Opioid Receptor Gene, Diagnostic Methods Using Said Alleles, and Methods of Treatment Based Thereon  
; FILE REFERENCE: 600-1-285N  
; CURRENT APPLICATION NUMBER: US/09/904,584  
; CURRENT FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: 60/218,300  
; PRIOR FILING DATE: 2000-07-14  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1154  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-09-904-584-3

Query Match	100.0%	Score 1154;	DB 11;	Length 1154;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1154;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ATGGACTCCCGATCCAGATCTTCCGGGGAGCGGCGCTTACCTGGCCCCGAGCGCC	60	
Db	1	ATGGACTCCCGATCCAGATCTTCCGGGGAGCGGCGCTTACCTGGCCCCGAGCGCC	60	
Qy	61	TGCTGCCCCCAACAGCAGCGCTGTGTTTCCCGGCTGGGCGGAGCCCGACAGCAACGCGC	120	





Qy 661 TGTGGGACCTCTTTCATGAAGATCTGGGTCTTTCATCTTTGCTTTCGTATCCCTGTCTC 720  
Db 661 TGTGGGACCTCTTTCATGAAGATCTGGGTCTTTCATCTTTGCTTTCGTATCCCTGTCTC 720  
Qy 721 ATCATCATCGTCTGTACACCTGATGATCTGCGTCTCAAGAGCGTCCGCTCTTCT 780  
Db 721 ATCATCATCGTCTGTACACCTGATGATCTGCGTCTCAAGAGCGTCCGCTCTTCT 780  
Qy 781 GGCTCCCGAGAGAAAGATCGCAACTGCGTAGGATCACAGACTGGTCTCGTGGTGGTG 840  
Db 781 GGCTCCCGAGAGAAAGATCGCAACTGCGTAGGATCACAGACTGGTCTCGTGGTGGTG 840  
Qy 841 GCAGTCTTCGTCTGTCTGAGTCCCATTCACATATTCATCTCTGGTAGGCTCTCGGG 900  
Db 841 GCAGTCTTCGTCTGTCTGAGTCCCATTCACATATTCATCTCTGGTAGGCTCTCGGG 900  
Qy 901 AGCACTCCCAACAGACAGCTGCTCTCTCAGCTATTTACTTCTGCATTCGCTTAGGCTAT 960  
Db 901 AGCACTCCCAACAGACAGCTGCTCTCTCAGCTATTTACTTCTGCATTCGCTTAGGCTAT 960  
Qy 961 ACCAAGTACCTGGAATCCATCTCTACGCTTTCTTGATGAAACTTCAAGCGGTGT 1020  
Db 961 ACCAAGTACCTGGAATCCATCTCTACGCTTTCTTGATGAAACTTCAAGCGGTGT 1020  
Qy 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGACAGCACTAGCAGATC 1080  
Db 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGACAGCACTAGCAGATC 1080  
Qy 1081 CGAATACAGTTACAGATCTGCTTACTTACAGGACATCGATGGGATGAATAACACAGTA 1140  
Db 1081 CGAATACAGTTACAGATCTGCTTACTTACAGGACATCGATGGGATGAATAACACAGTA 1140  
Qy 1141 TGACTAGTCGTGGA 1154  
Db 1141 TGACTAGTCGTGGA 1154

RESULT 3  
US-10-278-698-45  
; Sequence 45, Application US/10278698  
; Publication No. US20050037344A1  
; GENERAL INFORMATION:  
; APPLICANT: PathoArray GmbH  
; APPLICANT: Stuhlmüller, Bruno  
; APPLICANT: Haupl, Thomas  
; TITLE OF INVENTION: Nucleic Acid Array  
; FILE REFERENCE: 03002705  
; CURRENT APPLICATION NUMBER: US/10/278,698  
; CURRENT FILING DATE: 2002-10-23  
; NUMBER OF SEQ ID NOS: 1050  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 45  
; LENGTH: 1602  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-278-698-45

Query Match 99.9%; Score 1152.4; DB 19; Length 1602;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1153; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 ATGACTCCCCGATCCAGATCTTCCGGGGAGCGGGCCCTACTCGGCCCGGAGCGCC 60  
Db 376 ATGACTCCCCGATCCAGATCTTCCGGGGAGCGGGCCCTACTCGGCCCGGAGCGCC 435  
Qy 61 TGCTGCCCCCACAACAGCAGCGCTGTGTTCCCGGCTGGGCGGACCCGAGCAACGGC 120  
Db 436 TGCTGCCCCCACAACAGCAGCGCTGTGTTCCCGGCTGGGCGGACCCGAGCAACGGC 495  
Qy 121 AGCGCGGCTCGGAGGACCGCAGCTGGAGCCCGGCACATCTCCCGGCGCATCCCGGTC 180  
Db 496 AGCGCGGCTCGGAGGACCGCAGCTGGAGCCCGGCACATCTCCCGGCGCATCCCGGTC 555

Qy 181 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCTGGGCTTGTGGCAACTCGCTCGTC 240  
Db 556 ATCATCACGGCGGTCTACTCCGTAGTGTTCGTCTGGGCTTGTGGCAACTCGCTCGTC 615  
Qy 241 ATGTTCTGTATCATCCGATACAAAGATGAAGACAGCAACCAATTTACATATTTAAC 300  
Db 616 ATGTTCTGTATCATCCGATACAAAGATGAAGACAGCAACCAATTTACATATTTAAC 675  
Qy 301 CTGCTTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTTCAGAGTACGGTCTACTTG 360  
Db 676 CTGCTTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTTCAGAGTACGGTCTACTTG 735  
Qy 361 ATGAATTTCTGGCCTTTTGGGATGTCTGTGCAAGATAGTAAATTTCCATTGATTACTAC 420  
Db 736 ATGAATTTCTGGCCTTTTGGGATGTCTGTGCAAGATAGTAAATTTCCATTGATTACTAC 795  
Qy 421 AACATGTTTCAACAGATCTTTCACCTTGACCATGATGAGCGTGGACCGGTACATTGCCGTG 480  
Db 796 AACATGTTTCAACAGATCTTTCACCTTGACCATGATGAGCGTGGACCGGTACATTGCCGTG 855  
Qy 481 TGCACCCCGTGAAGGCTTTGGACTTCCGCACACCTTTGAAGGCAAAAGATCATCAATATC 540  
Db 856 TGCACCCCGTGAAGGCTTTGGACTTCCGCACACCTTTGAAGGCAAAAGATCATCAATATC 915  
Qy 541 TGCATCTGGCTGTCTGTCTCATCTGTGTTGGCATCTCTGCAATAGTCTTTGGAGGACCAAA 600  
Db 916 TGCATCTGGCTGTCTGTCTCATCTGTGTTGGCATCTCTGCAATAGTCTTTGGAGGACCAAA 975  
Qy 601 GTCAAGGAAGACGTGATGATCAATGAGTGTCTTTCAGATTCCTCCAGATGATGACTACTCC 660  
Db 976 GTCAAGGAAGACGTGATGATCAATGAGTGTCTTTCAGATTCCTCCAGATGATGACTACTCC 1035  
Qy 661 TGTGGGACCTCTTCAAGAGATCTGCTCTTCAATCTTTCGCTTCGTGATCCCTGTCCTC 720  
Db 1036 TGTGGGACCTCTTCAAGAGATCTGCTCTTCAATCTTTCGCTTCGTGATCCCTGTCCTC 1095  
Qy 721 ATCATCATCTGCTCTACACCTCTGATGATCTGCTCTCAAGAGCGTCCGCTCTCTTCT 780  
Db 1096 ATCATCATCTGCTCTACACCTCTGATGATCTGCTCTCAAGAGCGTCCGCTCTCTTCT 1155  
Qy 781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCAACAGACTGGTCTCGTGGTGGTG 840  
Db 1156 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCAACAGACTGGTCTCGTGGTGGTG 1215  
Qy 841 GCAGTCTTCTGCTGCTGCTGAGCTCCCATTCACATATTTCAATTCATTCCTGGTGGGCTCTGGG 900  
Db 1216 GCAGTCTTCTGCTGCTGCTGAGCTCCCATTCACATATTTCAATTCATTCCTGGTGGGCTCTGGG 1275  
Qy 901 AGCACTCCCAACAGCAGCTGCTCTCTCCAGCTATTTACTTTCGATTTGCTTAGGCTAT 960  
Db 1276 AGCACTCCCAACAGCAGCTGCTCTCTCCAGCTATTTACTTTCGATTCGCTTAGGCTAT 1335  
Qy 961 ACCAAGTACGTTGAGTCCCATTTCTCTA GCGCTTTCTTGATGAAAACCTTCAAGCGGTGT 1020  
Db 1336 ACCAAGTACGTTGAGTCCCATTTCTCTA GCGCTTTCTTGATGAAAACCTTCAAGCGGTGT 1395  
Qy 1021 TTCCGGGACTTCTGCTTTCCACTGAGATGAGGATGGAGCGGACAGCACTAGCAGATC 1080  
Db 1396 TTCCGGGACTTCTGCTTTCCACTGAGATGAGGATGGAGCGGACAGCACTAGCAGATC 1455  
Qy 1081 CGAATAACAGTTCAGGATCCTGCTTACCTGAGGACATCGATGGGATGAATAACACAGTA 1140  
Db 1456 CGAATAACAGTTCAGGATCCTGCTTACCTGAGGACATCGATGGGATGAATAACACAGTA 1515  
Qy 1141 TGACTAGTCGTGGA 1154  
Db 1516 TGACTAGTCGTGGA 1529

RESULT 4  
US-10-278-698-559  
; Sequence 559, Application US/10278698

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; Publication No. US20050037344A1
; GENERAL INFORMATION:
; APPLICANT: PathoArray GmbH
; APPLICANT: Stuhlmueller, Bruno
; APPLICANT: Haupl, Thomas
; TITLE OF INVENTION: Nucleic Acid Array
; FILE REFERENCE: 030027US
; CURRENT APPLICATION NUMBER: US/10/278,698
; CURRENT FILING DATE: 2002-10-23
; NUMBER OF SEQ ID NOS: 1050
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 559
; LENGTH: 1602
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-278-698-559

Query Match      99.9%; Score 1152.4; DB 19; Length 1602;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1153; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  ATGGACTCCCGATCCAGATCTTCCGCGGGAGCGCGGCCTTACCTGCGCCCGGAGCGCC 60
DB      376  ATGGACTCCCGATCCAGATCTTCCGCGGGAGCGCGGCCTTACCTGCGCCCGGAGCGCC 435

QY      61  TGCTGCCCCCAACAGCAGCGCTGTTCCCGGCTGGCGGAGCCCGACAGCAACGCG 120
DB      436  TGCTGCCCCCAACAGCAGCGCTGTTCCCGGCTGGCGGAGCCCGACAGCAACGCG 495

QY      121  AGCGCGGCTCGGAGGAGCGGAGCTGGAGCGCGGCACATCTCCCGCGGCATCCCGGTC 180
DB      496  AGCGCGGCTCGGAGGAGCGGAGCTGGAGCGCGGCACATCTCCCGCGGCATCCCGGTC 555

QY      181  ATCATCAGCGCGTCTACTCCGCTAGTGTTCGCTGGGCTTGGTGGGCAACTCGCTGGTC 240
DB      556  ATCATCAGCGCGTCTACTCCGCTAGTGTTCGCTGGGCTTGGTGGGCAACTCGCTGGTC 615

QY      241  ATGTCGTGATATCCGATACACAAAGATGAGAGCAAGCAACCAATTTACATATTAAAC 300
DB      616  ATGTCGTGATATCCGATACACAAAGATGAGAGCAAGCAACCAATTTACATATTAAAC 675

QY      301  CTGCTTTGGCAGATGCTTTAGTTACTACAAACATGCGCTTTCAGAGTACGGTCTACTTG 360
DB      676  CTGCTTTGGCAGATGCTTTAGTTACTACAAACATGCGCTTTCAGAGTACGGTCTACTTG 735

QY      361  ATGAATTCCTGGCTTTTGGGATGCTGTGCAAGATAGTAAATTTCCATTGATTACTAC 420
DB      736  ATGAATTCCTGGCTTTTGGGATGCTGTGCAAGATAGTAAATTTCCATTGATTACTAC 795

QY      421  AACATGTTCCACGATCTTTCACCTTGACCATGATGAGCGTGACCGCTACATTGCGGTG 480
DB      796  AACATGTTCCACGATCTTTCACCTTGACCATGATGAGCGTGAGCGGTACATTGCGGTG 855

QY      481  TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCCTTGAAGCAAGATCATCAATATC 540
DB      856  TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCCTTGAAGCAAGATCATCAATATC 915

QY      541  TGCATCTGGCTGCTGCTATCTGTTGGATCTCTGCAATATGCTTGGAGGACCAAA 600
DB      916  TGCATCTGGCTGCTGCTATCTGTTGGATCTCTGCAATATGCTTGGAGGACCAAA 975

QY      601  GTCAAGGAAGACGTCGATGTGCTTGGATGCTTCCAGATTTCCAGATGATGACTACTCC 660
DB      976  GTCAAGGAAGACGTCGATGTGCTTGGATGCTTCCAGATTTCCAGATGATGACTACTCC 1035

QY      661  TGGTGGGACCTCTTTCATGAAGATCTGGCTTTTCACTTTTGGCTTTCGATGCTCTC 720
DB      1036  TGGTGGGACCTCTTTCATGAAGATCTGGCTTTTCACTTTTGGCTTTCGATGCTCTC 1095

QY      721  ATCATATCGTCTGCTACACCGCTGATGATCTGCGTCTCAAGAGCGCGGCTCTTTCT 780
DB      1096  ATCATATCGTCTGCTACACCGCTGATGATCTGCGTCTCAAGAGCGCGGCTCTTTCT 1155

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RESULT 5

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US-09-904-584-2
; Sequence 2, Application US/09904584
; Publication No. US20040097704A1
; GENERAL INFORMATION:
; APPLICANT: Kreek, Mary Jeanne
; APPLICANT: Yuforov, Vadim
; APPLICANT: LaForge, Karl Steven
; TITLE OF INVENTION: Alleles of the Human Kappa Opioid
; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods Using Said Alleles, and
; TITLE OF INVENTION: Methods of Treatment Based Thereon
; FILE REFERENCE: 600-1-285N
; CURRENT APPLICATION NUMBER: US/09/904,584
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/218,300
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-904-584-2

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Query Match      99.7%; Score 1150.8; DB 11; Length 1154;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  ATGGACTCCCGATCCAGATCTTCCGCGGGAGCGCGGCCTTACCTGCGCCCGGAGCGCC 60
DB      1  ATGGACTCCCGATCCAGATCTTCCGCGGGAGCGCGGCCTTACCTGCGCCCGGAGCGCC 60

QY      61  TGCTGCCCCCAACAGCAGCGCTGTTCCCGGCTGGCGGAGCCCGACAGCAACGCG 120
DB      61  TGCTGCCCCCAACAGCAGCGCTGTTCCCGGCTGGCGGAGCCCGACAGCAACGCG 120

QY      121  AGCGCGGCTCGGAGGAGCGCGCAGCTGGAGCGCGGCACATCTCCCGGCGCATCCCGGTC 180
DB      121  AGCGCGGCTCGGAGGAGCGCGCAGCTGGAGCGCGGCACATCTCCCGGCGCATCCCGGTC 180

QY      181  ATCATCAGCGCGTCTACTCCGCTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC 240
DB      181  ATCATCAGCGCGTCTACTCCGCTAGTGTTCGTCGTGGGCTTGGTGGGCAACTCGCTGGTC 240

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Qy 241 ATGTTCTGATATCCGATACACAAAGATGAAGACAGCAACAAATTTACATATTAAC 300
Db 241 ATGTTCTGATCATCCGATACACAAAGATGAAGACAGCAACAAATTTACATATTAAC 300
Qy 301 CTGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCCCTTTTCAGAGTACGGTCTACTTG 360
Db 301 CTGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCCCTTTTCAGAGTACGGTCTACTTG 360
Qy 361 ATGAATTTCTGGCCCTTTTGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
Db 361 ATGAATTTCTGGCCCTTTTGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
Qy 421 AACATGTTTCCACGATCTTCCATTTGACCATGATGAGCGTGAACCGCTACATTTGCCGTG 480
Db 421 AACATGTTTCCACGATCTTCCATTTGACCATGATGAGCGTGAACCGCTACATTTGCCGTG 480
Qy 481 TGCCACCCCGTGAAGGCTTTGGACTTCCGACATCCGACACCCCTTGAAGGCAAGATCATCAATATC 540
Db 481 TGCCACCCCGTGAAGGCTTTGGACTTCCGACATCCGACACCCCTTGAAGGCAAGATCATCAATATC 540
Qy 541 TGCAATCTGGCTGCTGTCTGATCTGTGTCATCTGTGCAATAGTCTTGGAGGCAACAAA 600
Db 541 TGCAATCTGGCTGCTGTCTGATCTGTGTCATCTGTGCAATAGTCTTGGAGGCAACAAA 600
Qy 601 GTCAGGGAAGACGTGATGTCATGATGTCCTTTCAGATGTCCTTTCAGATGATGATCTCC 660
Db 601 GTCAGGGAAGACGTGATGTCATGATGTCCTTTCAGATGTCCTTTCAGATGATGATCTCC 660
Qy 661 TGCTGGGACCTTTTCATGAAGATCTGGCTCTTTCATCTTTCGCTTTCGATCCCTGCTC 720
Db 661 TGCTGGGACCTTTTCATGAAGATCTGGCTCTTTCATCTTTCGCTTTCGATCCCTGCTC 720
Qy 721 ATCATATCTGCTGTCTACACCTGATGATCTGCTGCTCTCAAGAGCGTCCGCTCTTCT 780
Db 721 ATCATATCTGCTGTCTACACCTGATGATCTGCTGCTCTCAAGAGCGTCCGCTCTTCT 780
Qy 781 GGCTCCCGAGAGAAGATCGCAACCTGCTGATGATCTGCTGCTCTCAAGAGCGTCCGCTG 840
Db 781 GGCTCCCGAGAGAAGATCGCAACCTGCTGATGATCTGCTGCTCTCAAGAGCGTCCGCTG 840
Qy 841 GCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Db 841 GCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Qy 901 AGCACTCTCCACAGACAGCTGCTCTCTCCAGCTATTTCTGCTGCTGCTGCTGCTGCTG 960
Db 901 AGCACTCTCCACAGACAGCTGCTCTCTCCAGCTATTTCTGCTGCTGCTGCTGCTGCTG 960
Qy 961 ACCAAGTACGCTGAATCCCATTTCTCTACGCTTTTCTGATGATAAACTTCAAGCGGTG 1020
Db 961 ACCAAGTACGCTGAATCCCATTTCTCTACGCTTTTCTGATGATAAACTTCAAGCGGTG 1020
Qy 1021 TTCCGGGACTTCTGCTTTCCTGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATG 1080
Db 1021 TTCCGGGACTTCTGCTTTCCTGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATG 1080
Qy 1081 CGAAATACAGTTACAGATCTGCTTACCTGAGGACATCGATGAGTGAATTAACACAGTA 1140
Db 1081 CGAAATACAGTTACAGATCTGCTTACCTGAGGACATCGATGAGTGAATTAACACAGTA 1140
Qy 1141 TGACTAGTCGTGA 1154
Db 1141 TGACTAGTCGTGA 1154

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RESULT 6  
 US-09-904-584-4  
 ; Sequence 4, Application US/09904584  
 ; Publication No. US20040097704A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kreek, Mary Jeanne  
 ; APPLICANT: Yuforov, Vadim  
 ; APPLICANT: LaForge, Karl Steven

; TITLE OF INVENTION: Alleles of the Human Kappa Opioid  
 ; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods Using Said Alleles, and  
 ; FILE REFERENCE: Methods of Treatment Based Thereon  
 ; CURRENT APPLICATION NUMBER: US/09/904,584  
 ; CURRENT FILING DATE: 2001-07-13  
 ; PRIOR FILING DATE: 60/218,300  
 ; NUMBER OF SEQ ID NOS: 7  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 4  
 ; LENGTH: 1154  
 ; TYPE: DNA  
 ; ORGANISM: homo sapiens  
 ; US-09-904-584-4

Query Match 99.7%; Score 1150.8; DB 11; Length 1154;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 ATGACTCTCCCGATCCAGATCTTCCGCGGGAGCGGGCCCTACTCTGCGCCCGAGGGCC 60
Db 1 ATGACTCTCCCGATCCAGATCTTCCGCGGGAGCGGGCCCTACTCTGCGCCCGAGGGCC 60
Qy 61 TGCTGCCCCCAACAGCAGCGCTGTTTCCCGGCTGGGCGGAGCCGACAGCAACGGC 120
Db 61 TGCTGCCCCCAACAGCAGCGCTGTTTCCCGGCTGGGCGGAGCCGACAGCAACGGC 120
Qy 121 AGCGCGGCTCGAGGAGCGGAGCTGGAGCGCGGACATCTCCCGGCGCATCCCGGTC 180
Db 121 AGCGCGGCTCGAGGAGCGGAGCTGGAGCGCGGACATCTCCCGGCGCATCCCGGTC 180
Qy 181 ATCATACGCGGCTACTCCGCTAGTGTCTGCTGGGCTTGGTGGGCACTCCGCTGTC 240
Db 181 ATCATACGCGGCTACTCCGCTAGTGTCTGCTGGGCTTGGTGGGCACTCCGCTGTC 240
Qy 241 ATGTTCTGATCATCCGATACAAAGATGAAGACAGCAACAAATTTACATATTAAC 300
Db 241 ATGTTCTGATCATCCGATACAAAGATGAAGACAGCAACAAATTTACATATTAAC 300
Qy 301 CTGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCCCTTTTCAGAGTACGGTCTACTTG 360
Db 301 CTGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCCCTTTTCAGAGTACGGTCTACTTG 360
Qy 361 ATGAATTTCTGGCCTTTTGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
Db 361 ATGAATTTCTGGCCTTTTGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420
Qy 421 AACATGTTTCCACGATCTTTCATCTGCTGATGATGAGCGTGAACCGCTACATTTGCCGTG 480
Db 421 AACATGTTTCCACGATCTTTCATCTGCTGATGATGAGCGTGAACCGCTACATTTGCCGTG 480
Qy 481 TGCCACCCCGTGAAGGCTTTGGACTTCCGACATCCGACACCCCTTGAAGGCAAGATCATCAATATC 540
Db 481 TGCCACCCCGTGAAGGCTTTGGACTTCCGACATCCGACACCCCTTGAAGGCAAGATCATCAATATC 540
Qy 541 TGCAATCTGGCTGCTGTCTGATGTCATCTGTGCAATAGTCTTGGAGGCAACAAA 600
Db 541 TGCAATCTGGCTGCTGTCTGATGTCATCTGTGCAATAGTCTTGGAGGCAACAAA 600
Qy 601 GTCAGGGAAGACGTGATGTCATGATGTCCTTTCAGATGTCCTTTCAGATGATGATCTCC 660
Db 601 GTCAGGGAAGACGTGATGTCATGATGTCCTTTCAGATGTCCTTTCAGATGATGATCTCC 660
Qy 661 TGCTGGGACCTTTTCATGAAGATCTGGCTCTTTCATCTTTCGCTTTCGATCCCTGCTC 720
Db 661 TGCTGGGACCTTTTCATGAAGATCTGGCTCTTTCATCTTTCGCTTTCGATCCCTGCTC 720
Qy 721 ATCATATCTGCTGTCTACACCTGATGATCTGCTGCTCTCAAGAGCGTCCGCTCTTCT 780
Db 721 ATCATATCTGCTGTCTACACCTGATGATCTGCTGCTCTCAAGAGCGTCCGCTCTTCT 780
Qy 781 GGCTCCCGAGAGAAGATCGCAACCTGCTGATGATCTGCTGCTCTCAAGAGCGTCCGCTG 840

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;; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods Using Said Alleles, and  
;; TITLE OF INVENTION: Methods of Treatment Based Thereon  
;; FILE REFERENCE: 600-1-285N  
;; CURRENT APPLICATION NUMBER: US/09/904,584  
;; CURRENT FILING DATE: 2001-07-13  
;; PRIOR APPLICATION NUMBER: 60/218,300  
;; PRIOR FILING DATE: 2000-07-14  
;; NUMBER OF SEQ ID NOS: 7  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 6  
;; LENGTH: 1154  
;; TYPE: DNA  
;; ORGANISM: homo sapiens  
US-09-904-584-6

Query Match 99.7%; Score 1150.8; DB 11; Length 1154;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGGACTCCCGATCCAGATCTTCGCGGGAGCGGGCCCTTACTCTGCGCCCCGAGCGCC 60  
Db 1 ATGGACTCCCGATCCAGATCTTCGCGGGAGCGGGCCCTTACTCTGCGCCCCGAGCGCC 60

Qy 61 TGCCTGCCCCCAACAGCAGCGCCCTGGTTTCCGGCTGGGGCGAGCCCGACAGCAACGGC 120  
Db 61 TGCCTGCCCCCAACAGCAGCGCCCTGGTTTCCGGCTGGGGCGAGCCCGACAGCAACGGC 120

Qy 121 AGCGCGCGCTCGGAGAGCGCAGCTGGAGCGCGCACATCTCCCGGCCATCCCGGTC 180  
Db 121 AGCGCGCGCTCGGAGAGCGCAGCTGGAGCGCGCACATCTCCCGGCCATCCCGGTC 180

Qy 181 ATCATCAGCGGGTCTACTCCGTAGTGTTCGTGCGGGCTTGGTGGGCAACTCGCTGTC 240  
Db 181 ATCATCAGCGGGTCTACTCCGTAGTGTTCGTGCGGGCTTGGTGGGCAACTCGCTGTC 240

Qy 241 ATGTTCTGTGATATCCGATACACAAAGATGAAGACAGCAACCAATTTACATATTAAC 300  
Db 241 ATGTTCTGTGATATCCGATACACAAAGATGAAGACAGCAACCAATTTACATATTAAC 300

Qy 301 CTGGCTTTGGCAGATGCTTTAGTTACTACACACCATGCCCTTTTCAGGTACCGTCTACTTG 360  
Db 301 CTGGCTTTGGCAGATGCTTTAGTTACTACACACCATGCCCTTTTCAGGTACCGTCTACTTG 360

Qy 361 ATGAATTCCTGGCCCTTTGGGGATGTGCTGTCAAGATAGTAATTTCCATTGATTACTAC 420  
Db 361 ATGAATTCCTGGCCCTTTGGGGATGTGCTGTCAAGATAGTAATTTCCATTGATTACTAC 420

Qy 421 AACATGTTTCCAGCATCTTCACTTGAACATGATGAGCGTGGACCGCTACATTGCGGTG 480  
Db 421 AACATGTTTCCAGCATCTTCACTTGAACATGATGAGCGTGGACCGCTACATTGCGGTG 480

Qy 481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCCTTGAAGGCAAGATCATCAATATC 540  
Db 481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCCTTGAAGGCAAGATCATCAATATC 540

Qy 541 TGCATCTGGCTGCTGTGCTCATCTGTGGCATCTCTGCAATAGTCTTGGAGGACCAAA 600  
Db 541 TGCATCTGGCTGCTGTGCTCATCTGTGGCATCTCTGCAATAGTCTTGGAGGACCAAA 600

Qy 601 GTACGGGAAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660  
Db 601 GTACGGGAAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660

Qy 661 TGGTGGGACCTTTCATCAAGATCTGCGTCTTCACTTTTGGCTTGGTATCCCTGCTC 720  
Db 661 TGGTGGGACCTTTCATCAAGATCTGCGTCTTCACTTTTGGCTTGGTATCCCTGCTC 720

Qy 721 ATCATCATCTGCTGTACACCTGATGATCTGCGTCTCAAGAGCGTCCGCTCTCTTCT 780  
Db 721 ATCATCATCTGCTGTACACCTGATGATCTGCGTCTCAAGAGCGTCCGCTCTCTTCT 780

Qy 781 GGCTCCCGAGAGAAGATGCAACCTGCTAGGATCACACAGACTGGTCTCGTGGTG 840  
Db 781 GGCTCCCGAGAGAAGATGCAACCTGCTAGGATCACACAGACTGGTCTCGTGGTG 840

Db 781 GGCTCCCGAGAGAAGATGCAACCTGCTAGGATCACACAGACTGGTCTCGTGGTG 840  
Qy 841 GCAGTCTTCGTGCTGCTGACTCCCATTCACATATTCATCTGCTGGAGGCTCTGGGG 900  
Db 841 GCGTCTTCGTGCTGCTGACTCCCATTCACATATTCATCTGCTGGAGGCTCTGGGG 900

Qy 901 AGCACTTCCACAGCAGCTGCTCTTCCAGCTATTTACTTTCTGATTTGCTTAGGCTAT 960  
Db 901 AGCACTTCCACAGCAGCTGCTCTTCCAGCTATTTACTTTCTGATTTGCTTAGGCTAT 960

Qy 961 ACCAACAGTAGCTGATCCCATTTCTAGCCCTTTCTTGATGAAAATTTCAAGCGGTG 1020  
Db 961 ACCAACAGTAGCTGATCCCATTTCTAGCCCTTTCTTGATGAAAATTTCAAGCGGTG 1020

Qy 1021 TTCCGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGACAGACTAGCAGAGTC 1080  
Db 1021 TTCCGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGACAGACTAGCAGAGTC 1080

Qy 1081 CGAAATACAGTTTCAAGTCTTCTAGCTAGGAGCATCGATGGATGAATAAACCACTA 1140  
Db 1081 CGAAATACAGTTTCAAGTCTTCTAGCTAGGAGCATCGATGGATGAATAAACCACTA 1140

Qy 1141 TGACTAGTCTGGA 1154  
Db 1141 TGACTAGTCTGGA 1154

RESULT 9  
US-09-904-584-7  
; Sequence 7, Application US/09904584  
; Publication No. US20040097704A1  
; GENERAL INFORMATION:  
; APPLICANT: Kreek, Mary Jeanne  
; APPLICANT: Yuforov, Vadim  
; APPLICANT: LaForge, Karl Steven  
; TITLE OF INVENTION: Alleles of the Human Kappa Opioid  
; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods Using Said Alleles, and  
; TITLE OF INVENTION: Methods of Treatment Based Thereon  
; FILE REFERENCE: 600-1-285N  
; CURRENT APPLICATION NUMBER: US/09/904,584  
; CURRENT FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: 60/218,300  
; PRIOR FILING DATE: 2000-07-14  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 1154  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-09-904-584-7

Query Match 99.7%; Score 1150.8; DB 11; Length 1154;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGGACTCCCGATCCAGATCTTCGCGGGAGCGGGCCCTTACTCTGCGCCCCGAGCGCC 60  
Db 1 ATGGACTCCCGATCCAGATCTTCGCGGGAGCGGGCCCTTACTCTGCGCCCCGAGCGCC 60

Qy 61 TGCCTGCCCCCAACAGCAGCGCCCTGGTTTCCGGCTGGGGCGAGCCCGACAGCAACGGC 120  
Db 61 TGCCTGCCCCCAACAGCAGCGCCCTGGTTTCCGGCTGGGGCGAGCCCGACAGCAACGGC 120

Qy 121 AGCGCGCGCTCGGAGAGCGCAGCTGGAGCGCGCACATCTCCCGGCCATCCCGGTC 180  
Db 121 AGCGCGCGCTCGGAGAGCGCAGCTGGAGCGCGCACATCTCCCGGCCATCCCGGTC 180

Qy 181 ATCATCAGCGGGTCTACTCCGTAGTGTTCGTGCGGGCTTGGTGGGCAACTCGCTGTC 240  
Db 181 ATCATCAGCGGGTCTACTCCGTAGTGTTCGTGCGGGCTTGGTGGGCAACTCGCTGTC 240

Qy 241 ATGTTCTGTGATATCCGATACACAAAGATGAAGACAGCAACCAATTTACATATTAAC 300  
Db 241 ATGTTCTGTGATATCCGATACACAAAGATGAAGACAGCAACCAATTTACATATTAAC 300



241 ATGTTCTGTGATCCGATACACAAAGATGAAGACAGACCAACCAATTTACATATTTAAAC 300  
 301 CTGGCTTTGGCAGATCGTTTGTAGTACTACAAACATGCCCTTTTCAGAGTACGCTTACTTTG 360  
 301 CTGGCTTTGGCAGATCGTTTGTAGTACTACAAACATGCCCTTTTCAGAGTACGCTTACTTTG 360  
 361 ATGAATTTCTGGCTTTTGGGATGCTGTGCAAGATAGTAATTTCCATTTGATTACTAC 420  
 361 ATGAATTTCTGGCTTTTGGGATGCTGTGCAAGATAGTAATTTCCATTTGATTACTAC 420  
 421 AACATGTTTCCACAGCATCTTTCACTTTGACATGATGAGCGTGACCGCTACATATTC 480  
 421 AACATGTTTCCACAGCATCTTTCACTTTGACATGATGAGCGTGACCGCTACATATTC 480  
 481 TGCCACCCCGTGAAGCTTTTGGACTTTCCGACACACCTTTGAAGCAAGATCATCATATTC 540  
 481 TGCCACCCCGTGAAGCTTTTGGACTTTCCGACACACCTTTGAAGCAAGATCATCATATTC 540  
 541 TGATCTGGCTGTGCTGCTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGCACAAA 600  
 541 TGATCTGGCTGTGCTGCTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGCACAAA 600  
 601 GTGAGGAAGACGTCGATGTCATTGAGTGCTCTTCCAGTTCCTCCAGATGATGACTACTCC 660  
 601 GTGAGGAAGACGTCGATGTCATTGAGTGCTCTTCCAGTTCCTCCAGATGATGACTACTCC 660  
 661 TGCTGGGACCTCTTCAAGATCTGCGTCTTCACTTTTGCCTTCTGATCCCTGTCCTC 720  
 661 TGCTGGGACCTCTTCAAGATCTGCGTCTTCACTTTTGCCTTCTGATCCCTGTCCTC 720  
 721 ATCATCATCTGCTGTACACCTTGATGATCTCGCTCTCAAGAGCGTCCGGCTCTTTCT 780  
 721 ATCATCATCTGCTGTACACCTTGATGATCTCGCTCTCAAGAGCGTCCGGCTCTTTCT 780  
 781 GGCTCCGAGAGAAAGATCGAACCTGCGTAGGATCAACAGACTGCTGTGCTGCTG 840  
 781 GGCTCCGAGAGAAAGATCGAACCTGCGTAGGATCAACAGACTGCTGTGCTGCTG 840  
 841 GCAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
 841 GCAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
 901 AGCACCTTCCACAGCAGCTGCTCTCTCCAGCTATTACTTTCTGCAATTTGCTTAGGCTAT 960  
 901 AGCACCTTCCACAGCAGCTGCTCTCTCCAGCTATTACTTTCTGCAATTTGCTTAGGCTAT 960  
 961 ACCAAGATGAGCTGAATCCATCTCTAGCCTTTCTGATGAAATCTTCAAGCGGTGT 1020  
 961 ACCAAGATGAGCTGAATCCATCTCTAGCCTTTCTGATGAAATCTTCAAGCGGTGT 1020  
 1021 TTCGGGACTTCTGCTTCCACTGAAGATGAGGATGAGCGGCGAGAGCTAGCAGATC 1080  
 1021 TTCGGGACTTCTGCTTCCACTGAAGATGAGGATGAGCGGCGAGAGCTAGCAGATC 1080  
 1081 CGAAATACAGTTTCAAGATCTGCTTACCTGAGGACATCATGCGGATGATTAACACAGTA 1140  
 1081 CGAAATACAGTTTCAAGATCTGCTTACCTGAGGACATCATGCGGATGATTAACACAGTA 1140  
 1141 TGACTAGTCGTGA 1154  
 1141 TGACTAGTCGTGA 1154

RESULT 10  
 US-10-225-567A-147  
 ; Sequence 147, Application US/10225567A  
 ; Publication No. US20030113798A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: LifeSpan Biosciences  
 ; APPLICANT: Brown, Joseph P.  
 ; APPLICANT: Burmer, Glenna C.  
 ; APPLICANT: Roush, Christine L.  
 ; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS

FILE REFERENCE: 1920-4-4  
 ; CURRENT APPLICATION NUMBER: US/10/225,567A  
 ; CURRENT FILING DATE: 2001-12-19  
 ; PRIOR APPLICATION NUMBER: 60/257,144  
 ; PRIOR FILING DATE: 2000-12-19  
 ; NUMBER OF SEQ ID NOS: 2292  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 147  
 ; LENGTH: 1182  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; ORGANISM: Homo sapiens  
 ; US-10-225-567A-147

Query Match 99.2%; Score 1144.4; DB 15; Length 1182;  
 Best Local Similarity 99.5%; Pred. No. 0;  
 Matches 1148; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 1 ATGGAATCCCCGATCCAGATCTTCCGCGGGAGCGGGCCCTTACCTGCGCCCGGAGCGCC 60  
 14 ATGGAATCCCCGATCCAGATCTTCCGCGGGAGCGCTGCGCCTTACCTGCGCCCGGAGCGCC 73  
 61 TGCTGCCCCCAACAGCAGCGCCTTGGTTTCCCGGCTGGGCGGAGCGCCGACAGCAACGCG 120  
 74 TGCTGCCCCCAACAGCAGCGCCTTGGTTTCCCGGCTGGGCGGAGCGCCGACAGCAACGCG 133  
 121 AGCGCGGCTCGAGAGCGCGCAGCTGGAGCGCGGCGCACATCTCCCGGCGCATCCCGGTC 180  
 134 AGCGCGGCTCGAGAGCGCGCAGCTGGAGCGCGGCGCACATCTCCCGGCGCATCCCGGTC 193  
 181 ATCATCAGCGGCTTACTCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
 194 ATCATCAGCGGCTTACTCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 253  
 241 ATGTTCTGTGATCATCCGATACACAAAGATGAAGACAGACCAACCAATTTACATATTTAA 300  
 254 ATGTTCTGTGATCATCCGATACACAAAGATGAAGACAGACCAACCAATTTACATATTTAA 313  
 301 CTGGCTTTGGCAGATCGTTTGTAGTACTACAAACATGCCCTTTTCAGAGTACGCTTACTTTG 360  
 314 CTGGCTTTGGCAGATCGTTTGTAGTACTACAAACATGCCCTTTTCAGAGTACGCTTACTTTG 373  
 361 ATGAATTTCTGGCTTTTGGGATGCTGTGCAAGATAGTAATTTCCATTTGATTACTAC 420  
 374 ATGAATTTCTGGCTTTTGGGATGCTGTGCAAGATAGTAATTTCCATTTGATTACTAC 433  
 421 AACATGTTTCCACAGCATCTTCACTTTGACATGATGAGCGTGACCGCTACATTTGCCGTG 480  
 434 AACATGTTTCCACAGCATCTTCACTTTGACATGATGAGCGTGACCGCTACATTTGCCGTG 493  
 481 TGCCACCCCGTGAAGCTTTTGGACTTTCCGACACACCTTTGAAGCAAGATCATCATATTC 540  
 494 TGCCACCCCGTGAAGCTTTTGGACTTTCCGACACACCTTTGAAGCAAGATCATCATATTC 553  
 541 TGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
 554 TGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 613  
 601 GTCAGGAGAGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
 614 GTCAGGAGAGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 673  
 661 TGCTGGGACCTCTTCAAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720  
 674 TGCTGGGACCTCTTCAAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 733  
 721 ATCATCATCTGCTGTACACCTTGATGATCTCGCTCTCAAGAGCGTCCGGCTCTCTTTCT 780  
 734 ATCATCATCTGCTGTACACCTTGATGATCTCGCTCTCAAGAGCGTCCGGCTCTCTTTCT 793  
 781 GGCTCCGAGAGAAAGATCGAACCTGCGTAGGATCAACAGACTGCTGTGCTGCTGCTGCTG 840  
 794 GGCTCCGAGAGAAAGATCGAACCTGCGTAGGATCAACAGACTGCTGTGCTGCTGCTGCTG 853





Db 1094 CGAAATACAGTTTCAGGATCTCTTACCTGAGGACATCGATGGATGAATAAACCGAGTA 1153

Qy 1141 TGACTAGTCGTGGA 1154

Db 1154 TGACTAGTCGTGGA 1167

RESULT 12

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US-10-305-720-1417
; Sequence 1417, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1417
; LENGTH: 1182
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g532059
US-10-305-720-1417

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Query Match	99.2%	Score 1144.4	DB 17	Length 1182
Best Local Similarity	99.5%	Pred. No. 0		
Matches 1148	Conservative 0	Mismatches 6	Indels 0	Gaps 0
Qy	1	ATGAGCTCCCGGATCCAGATCTTCCGGGGGAGCGGGCCCTACTCTGCGCCCGAGCGCC	60	
Db	14	ATGGAATCCCGGATTCAGATCTTCGGGGGAGCTTGGCCCTACTCTGCGCCCGAGCGCC	73	
Qy	61	TGCTGCGCCCGCAACACAGAGCGCTGGTTTCCGGGCTGGGCGGAGCCGACAGCAACGGC	120	
Db	74	TGCTGCGCCCGCAACACAGAGCGCTGGTTTCCGGGCTGGGCGGAGCCGACAGCAACGGC	133	
Qy	121	AGCGCCGGCTCGGAGGAGCGGACGCTGGAGCGCGCGCACATCTCCCGGGCATCCCGGCT	180	
Db	134	AGCGCCGGCTCGGAGGAGCGGACGCTGGAGCGCGCGCACATCTCCCGGGCATCCCGGCT	193	
Qy	181	ATCATCAAGCGGCTACTTCGTAAGTGTTCGTCTGGGCTTGGTGGGCAACTCGCTGGTC	240	
Db	194	ATCATCAAGCGGCTACTTCGTAAGTGTTCGTCTGGGCTTGGTGGGCAACTCGCTGGTC	253	
Qy	241	ATGTTCTGTGATCATCCGATACACAAAGATGAAGACAGCAACCAATTTTACATATTTAAC	300	
Db	254	ATGTTCTGTGATCATCCGATACACAAAGATGAAGACAGCAACCAATTTTACATATTTAAC	313	
Qy	301	CTGCTTTTGGCAGATGCTTTAGTTTACTACAAACCATGCCCTTTCAGAGTACGGTCTACTTG	360	
Db	314	CTGCTTTTGGCAGATGCTTTAGTTTACTACAAACCATGCCCTTTCAGAGTACGGTCTACTTG	373	
Qy	361	ATGAATTCCTGGCCCTTTTGGGGATGCTGTGCAAGATAGTAATTTCCATTGATTACTAC	420	
Db	374	ATGAATTCCTGGCCCTTTTGGGGATGCTGTGCAAGATAGTAATTTCCATTGATTACTAC	433	
Qy	421	AACATGTTACCCAGCATCTTCACCTTGACCATATGAGCGGTGGACCGCTACATTCGCGTG	480	
Db	434	AACATGTTACCCAGCATCTTCACCTTGACCATATGAGCGGTGGACCGCTACATTCGCGTG	493	
Qy	481	TGCCACCCCGTGAAGGCTTTGGACTTCGGACACCCCTTGAAGGCAAGATCATCAATATC	540	
Db	494	TGCCACCCCGTGAAGGCTTTGGACTTCGGACACCCCTTGAAGGCAAGATCATCAATATC	553	
Qy	541	TGCAATCTGGGCTGTGCTCATCTCTGTTTGGCATCTCTCTGCAATAGTCTTGGAGGCCACCAA	600	

RESULT 13  
US-10-283-975A-80  
Sequence 80, Application US/10283975A  
Publication No. US20040110792A1  
GENERAL INFORMATION:  
APPLICANT: Ortho-Clinical Diagnostics, Inc.  
TITLE OF INVENTION: Methods For Assessing and Treating Leukemia  
FILE REFERENCE: CDS 293 PCT  
CURRENT APPLICATION NUMBER: US/10/283,975A  
CURRENT FILING DATE: 2002-10-30  
PRIOR APPLICATION NUMBER: 60/340,938  
PRIOR FILING DATE: 2001-10-30  
PRIOR APPLICATION NUMBER: 60/338,997  
PRIOR FILING DATE: 2001-10-30  
PRIOR APPLICATION NUMBER: 60/340,081  
PRIOR FILING DATE: 2001-10-30  
PRIOR APPLICATION NUMBER: 60/341,012  
PRIOR FILING DATE: 2001-10-30  
NUMBER OF SEQ ID NOS: 900  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 80  
LENGTH: 1182  
TYPE: DNA  
ORGANISM: HUMAN  
US-10-283-975A-80

Query Match	99.2%	Score 1144.4	DB 18	Length 1182
Best Local Similarity	99.5%	Pred. No. 0		
Matches 1148	Conservative	0	Mismatches 6	Indels 0
				Gaps 0

Qy 1 ATGGACTCCCGATCCAGATCTTCGGCGGGAGCGGGCCCTACTCTGGCGCCCGGAGCGCC 60  
 Db 14 ATGGAATCCCGATTCAGATCTTCGGCGGGAGCGCTGGCCCTACTCTGGCGCCCGGAGCGCC 73  
 Qy 61 TGCCTGCCCGCCCAACAGCAGCGCTGTTTCCGCGTGGCGGAGCGCCGAGCAACGCGC 120  
 Db 74 TGCCTGCCCGCCCAACAGCAGCGCTGTTTCCGCGTGGCGGAGCGCCGAGCAACGCGC 133  
 Qy 121 AGCGCGGCTCGGAGGAGCGCAGCTGGAGCGCGGACATCTCCCGCGCCCATCCCGGTC 180  
 Db 134 AGCGCGGCTCGGAGGAGCGCAGCTGGAGCGCGGACATCTCCCGCGCCCATCCCGGTC 193  
 Qy 181 ATCATCAGCGGCTTACTCTCGTAGTGTTCGTGGGCTTGGTGGGCACTCGTGGTC 240  
 Db 194 ATCATCAGCGGCTTACTCTCGTAGTGTTCGTGGGCTTGGTGGGCACTCGTGGTC 253  
 Qy 241 ATGTTCTGATCATCCGATACACAAAGATGAAGACAGCAACCAATTTACATATTAAC 300  
 Db 254 ATGTTCTGATCATCCGATACACAAAGATGAAGACAGCAACCAATTTACATATTAAC 313  
 Qy 301 CTGGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCCCTTTTCAGAGTACGGTCTACTTG 360  
 Db 314 CTGGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCCCTTTTCAGAGTACGGTCTACTTG 373  
 Qy 361 ATGAATCTCTGGCTTTGGGATGCTGTGCAAGATAGTAATTTCAATTTGATTAATAC 420  
 Db 374 ATGAATCTCTGGCTTTGGGATGCTGTGCAAGATAGTAATTTCAATTTGATTAATAC 433  
 Qy 421 AACATGTTTACACAGCATCTTACCTTGACCATGATGAGCGTGGACCGTACATTTCCGCTG 480  
 Db 434 AACATGTTTACACAGCATCTTACCTTGACCATGATGAGCGTGGACCGTACATTTCCGCTG 493  
 Qy 481 TGCCACCCCGTGAAGGCTTTGAGATCTCCGACACCCCTTGAAGGCAAGATCATCAATATC 540  
 Db 494 TGCCACCCCGTGAAGGCTTTGAGATCTCCGACACCCCTTGAAGGCAAGATCATCAATATC 553  
 Qy 541 TGCATCTGGCTGTCTGCTATCTGTTGGCATCTGCAATAGTCTTGGAGGACCAAA 600  
 Db 554 TGCATCTGGCTGTCTGCTATCTGTTGGCATCTGCAATAGTCTTGGAGGACCAAA 613  
 Qy 601 GTGAGGAGAGCGTGAAGTCTTATGAGTGTCTTGGATCTTCCAGATGATGATGATCTCC 660  
 Db 614 GTGAGGAGAGCGTGAAGTCTTATGAGTGTCTTGGATCTTCCAGATGATGATGATCTCC 673  
 Qy 661 TGGTGGGACCTCTTATGAAGATCTGCTCTTCTATCTTGGCTTCTGATCCCTGTCTCTC 720  
 Db 674 TGGTGGGACCTCTTATGAAGATCTGCTCTTCTATCTTGGCTTCTGATCCCTGTCTCTC 733  
 Qy 721 ATCATCATCTGCTGTCTACACCTGATGATCTGCTGTCTCAAGAGCGTCCGCTCTTCT 780  
 Db 734 ATCATCATCTGCTGTCTACACCTGATGATCTGCTGTCTCAAGAGCGTCCGCTCTTCT 793  
 Qy 781 GGCTCCCGAGAGAGATCGCAACCTGGTAGGATCACCAGACTGGTCTGGTGGTGGTG 840  
 Db 794 GGCTCCCGAGAGAGATCGCAACCTGGTAGGATCACCAGACTGGTCTGGTGGTGGTG 853  
 Qy 841 GCAGTCTTCTGCTGTCTGAGTCCCATTCACATATTCATCTTGGTGGAGGCTCTGGG 900  
 Db 854 GCGGTTTCTGCTGTCTGAGTCCCATTCACATATTCATCTTGGTGGAGGCTCTGGG 913  
 Qy 901 AGCACCTCCACAGACAGCTGCTCTCTCCAGCTATTACTTCTGCAATTTAGGCTAT 960  
 Db 914 AGCACCTCCACAGACAGCTGCTCTCTCCAGCTATTACTTCTGCAATTTAGGCTAT 973  
 Qy 961 ACCAAGTAGCTGAATCCCATCTCTAGCGCTTTCTTGTATGAAAACTTCAAGGGGTGT 1020  
 Db 974 ACCAAGTAGCTGAATCCCATCTCTAGCGCTTTCTTGTATGAAAACTTCAAGGGGTGT 1033  
 Qy 1021 TTCCGGGACTTCTGCTTTCCATGAGATGAGGATGAGCGGAGCACTAGCAGAGTC 1080  
 Db 1034 TTCCGGGACTTCTGCTTTTCCATGAGATGAGGATGAGCGGAGCACTAGCAGAGTC 1093  
 Qy 1081 CGAATAACAGTTTACGGATCTCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCAAGTA 1140

Db 1094 CGAATAACAGTTTACGGATCTCTGCTTACCTGAGGACATCGATGGATGAATAAACCAAGTA 1153  
 Qy 1141 TGACTAGTCGTGGA 1154  
 Db 1154 TGACTAGTCGTGGA 1167  
 RESULT 14  
 US-10-318-661-1  
 ; Sequence 1, Application US/10318661  
 ; Publication No. US20030167476A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Conklin, Bruce R.  
 ; TITLE OF INVENTION: Selective Target Cell Activation By  
 ; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated  
 ; TITLE OF INVENTION: Superiorly By Synthetic Ligand  
 ; FILE REFERENCE: UCAL-049CIP2  
 ; CURRENT APPLICATION NUMBER: US/10/318,661  
 ; CURRENT FILING DATE: 2003-05-05  
 ; PRIOR APPLICATION NUMBER: US 09/341,446  
 ; PRIOR FILING DATE: 1999-12-20  
 ; PRIOR APPLICATION NUMBER: PCT/US97/05334  
 ; PRIOR FILING DATE: 1997-03-25  
 ; PRIOR APPLICATION NUMBER: US 08/622,348  
 ; PRIOR FILING DATE: 1996-03-26  
 ; NUMBER OF SEQ ID NOS: 28  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 1143  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-318-661-1  
 Query Match 98.9%; Score 1141.4; DB 16; Length 1143;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1142; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 ATGAGCTCCCGATCCAGATCTTCCGCGGGAGCGGGCCCTACTCTGGCGCCCGGAGCGCC 60  
 Db 1 ATGAGCTCCCGATCCAGATCTTCCGCGGGAGCGGGCCCTACTCTGGCGCCCGGAGCGCC 60  
 Qy 61 TGCCTGCCCGCCCAACAGCAGCGCTGTTTCCGCGTGGCGGAGCGCCGAGCAACGCGC 120  
 Db 61 TGCCTGCCCGCCCAACAGCAGCGCTGTTTCCGCGTGGCGGAGCGCCGAGCAACGCGC 120  
 Qy 121 AGCGCGGCTCGGAGGAGCGCAGCTGGAGCGCGGACATCTCCCGCGCCCATCCCGGTC 180  
 Db 121 AGCGCGGCTCGGAGGAGCGCAGCTGGAGCGCGGACATCTCCCGCGCCCATCCCGGTC 180  
 Qy 181 ATCATCAGCGGCTTACTCTCGTAGTGTTCGTGGGCTTGGTGGGCACTCGCTGGTC 240  
 Db 181 ATCATCAGCGGCTTACTCTCGTAGTGTTCGTGGGCTTGGTGGGCACTCGCTGGTC 240  
 Qy 241 ATGTTCTGATCATCCGATACACAAAGATGAAGACAGCAACCAATTTACATATTAAC 300  
 Db 241 ATGTTCTGATCATCCGATACACAAAGATGAAGACAGCAACCAATTTACATATTAAC 300  
 Qy 301 CTGGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCCCTTTTCAGAGTACGGTCTACTTG 360  
 Db 301 CTGGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCCCTTTTCAGAGTACGGTCTACTTG 360  
 Qy 361 ATGAATTTCTGGCGCTTTTGGGATGCTGTGCAAGATAGTAATTTCAATTTGATTAATAC 420  
 Db 361 ATGAATTTCTGGCGCTTTTGGGATGCTGTGCAAGATAGTAATTTCAATTTGATTAATAC 420  
 Qy 421 AACATGTTTACACAGCATCTTCACTTACCAACCATGCCCTTTTCAGAGTACGGTCTACTTG 480  
 Db 421 AACATGTTTACACAGCATCTTCACTTACCAACCATGCCCTTTTCAGAGTACGGTCTACTTG 480  
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 841 GCAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
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RESULT 15  
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 ; Sequence 3, Application US/10318661  
 ; Publication No. US2003016746A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Conklin, Bruce R.  
 ; TITLE OF INVENTION: Selective Target Cell Activation By  
 ; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated  
 ; TITLE OF INVENTION: Superiorly By Synthetic Ligand  
 ; FILE REFERENCE: UCAL-049CIP2  
 ; CURRENT APPLICATION NUMBER: US/10/318,661  
 ; CURRENT FILING DATE: 2003-05-05  
 ; PRIOR APPLICATION NUMBER: US 09/341,446  
 ; PRIOR FILING DATE: 1999-12-20  
 ; PRIOR APPLICATION NUMBER: PCT/US97/05334  
 ; PRIOR FILING DATE: 1997-03-25  
 ; PRIOR APPLICATION NUMBER: US 08/622,348  
 ; PRIOR FILING DATE: 1996-03-26  
 ; NUMBER OF SEQ ID NOS: 28  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 3  
 ; LENGTH: 1284  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: modified KOR  
 US-10-318-661-3

Query Match 98.5%; Score 1136.2; DB 16; Length 1284;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 1138; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 2 TGGACTCCCGGATCCAGATCTTCCGCGGGAGCCGCGCCCTACCTGCGCCCGAGCGCCT 61  
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 62 GCTGCGCCCGGATCCAGATCTTCCGCGGGAGCCGCGCCCTACCTGCGCCCGAGCGCCT 121  
 173 GCTGCGCCCGGATCCAGATCTTCCGCGGGAGCCGCGCCCTACCTGCGCCCGAGCGCCT 232  
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 182 TCATCA CGCGGCTCTACTCCGCTAGTCTTCCGCGGGAGCCGCGCCCTACCTGCGGTCA 241  
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 242 TGTTCGTGATCATCCGATACACAAAGATGAAAGACAGCAACCAACATTTACATATTTAAC 301  
 353 TGTTCGTGATCATCCGATACACAAAGATGAAAGACAGCAACCAACATTTACATATTTAAC 412  
 302 TGGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCGCTTTCAGAGTACGGTCTACTTGA 361  
 413 TGGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCGCTTTCAGAGTACGGTCTACTTGA 472  
 362 TGAATTCCTGGCTTTTGGGATGCTGTCGAAAGATAGTAATTTCCATTTGATTTACTACA 421  
 473 TGAATTCCTGGCTTTTGGGATGCTGTCGAAAGATAGTAATTTCCATTTGATTTACTACA 532  
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 533 ACATGTTTACCAGCATCTTACCTTGACCATGATGAGCGTGGACCGCTACATTTGCCGTCT 592  
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 593 GCCACCCCGTGAAGGCTTTGGAGCTTCCGACACACCTTTGAAGGCAAGATCATCAATATCT 652  
 542 GCATCTGGCTGCTGCTCATCTGTTGGCATCTCTGCAATAGTCTCTTGGAGGACCAAG 601  
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 962 CCACAGTAGCTGATCCCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1021  
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Qy	1022	TCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCGAGCACTAGCAGAGTCC	1081
Db	1133	TCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGCGAGCACTAGCAGAGTCC	1192
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Db	1193	GAATACAGTTCAGGATCCTGCTTACCTGAGGACATCGATGGGATGAATAACCACTAT	1252
Qy	1142	G	1142
Db	1253	G	1253

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 Job time : 769.333 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 6, 2005, 12:28:42 ; Search time 4384.33 Seconds  
(without alignments)  
10018.893 Million cell updates/sec

Title: US-09-904-584-3

Perfect score: 1154

Sequence: 1 atggactcccgatccagat.....ccagatgactagtcgtgga 1154

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_hc:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_ges1:\*

9: gb\_ges2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	805.2	69.8	895	6	CB565888
2	581.8	50.4	762	7	CO960667
3	518.8	45.0	784	7	CO960682
4	470.6	40.8	837	7	CF593603
5	466.4	40.4	480	5	BK092912
6	432.4	37.5	2405	3	AK038389
7	421.6	36.5	4022	3	AK043873
8	367.8	31.9	2919	3	AK038620
9	367.8	31.9	2959	3	AK079529
10	352	30.5	879	9	AY410745
11	335.6	29.1	2940	3	AK044178
12	327.4	28.4	2974	3	AK043275
13	327	28.3	3101	3	AK031926
14	325.8	28.2	879	9	AY410747
15	309.8	26.8	1053	9	CNS04C2T
16	277.6	24.1	775	5	BX874804
17	274.2	23.8	787	7	CN439929
18	270.2	23.4	917	5	BU219878
19	269.8	23.4	888	2	BF676176
20	264.4	22.9	579	5	BP214141
21	263.8	22.9	579	5	BP213719
22	239.8	20.8	682	2	BS588668
23	231.2	20.0	682	2	AY410746
24	228	19.8	1176	9	AY400827

25	227.4	19.7	389	2	BE649947
26	225	19.5	1176	9	AY400829
27	225	19.5	2014	3	AK046464
28	224.6	19.5	980	4	BW543468
29	223	19.3	632	2	BB641725
30	221.4	19.2	1006	9	AY400676
31	217.6	18.9	784	5	BQ179053
32	215.8	18.7	750	7	CO934661
33	214.8	18.6	1006	9	AY400674
34	214.8	18.6	2048	3	CF593522
35	214	18.5	429	4	BM342951
36	213	18.5	836	9	CNS02261
37	213	18.5	866	6	CD246184
38	212.2	18.4	2432	3	AK051189
39	211	18.3	531	9	CE517843
40	208.6	18.1	877	9	CNS028C2
41	207.8	18.0	697	5	BUL39251
42	207.8	18.0	757	5	BUE14716
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#### ALIGNMENTS

RESULT 1  
LOCUS CB565888  
DEFINITION AGENCOURT 12691503 NIH\_MGC 146 Homo sapiens cDNA clone  
IMAGE:6519213 5', mRNA sequence.  
ACCESSION CB565888  
VERSION CB565888.1 GI:29485418  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 895)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Guthrie cDNA Resource Center  
CDNA Library Preparation: Guthrie cDNA Resource Center  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at:  
http://image.llnl.gov  
Plate: IRBF001 row: f column: 09  
High quality sequence stop: 763.

#### FEATURES

##### source

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/db\_xref="taxon:9606"  
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/tissue\_type="mixed"  
/lab\_host="DH10B (TI-phage-resistant)"  
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/note="Vector: pCDNA3.1; Site 1: multiple; Site 2: multiple; ORF's were PCR-amplified (from IMAGE clones or from commercially available cDNA libraries) and cloned by the Guthrie cDNA Resource Center (www.guthrie.org/cdna) into pCDNA3.1. For specific information on cloning sites (which vary by clone), please refer to the Guthrie website, using the Guthrie ID given in the file ftp://image.llnl.gov/image.rearrayed\_plates/IRBF.presv.dat a. Note: this is a NIH\_MGC Library."

#### ORIGIN



Query Match		69.8%; Score 805.2; DB 6; Length 895;
Best Local Similarity		97.1%; Pred. No. 3e-200;
Matches		841; Conservative 0; Mismatches 23; Indels 2; Gaps 2;
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QY	61	TGCTGCCCCCACAAGCAGCGCTGGTTCCCGCTGGCGGAGCCCGACAGCAACGCG 120
Db	62	TGCTGCCCCCACAAGCAGCGCTGGTTCCCGCTGGCGGAGCCCGACAGCAACGCG 121
QY	121	AGCGCGGCTCGGAGGACGCGAGCTGGAGCCCGCACATCTCCCGCGCCATCCCGGTC 180
Db	122	AGCGCGGCTCGGAGGACGCGAGCTGGAGCCCGCACATCTCCCGCGCCATCCCGGTC 181
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Db	242	ATGTTCTGTATCTCCGATACCAAGATGAAGACAGCAACCAATTACATATTAAAC 301
QY	301	CTGGCTTTGGCAGATGCTTTAGTTACTACCAACCATGCCCTTTCCAGAGTACGGTCTACTTG 360
Db	302	CTGGCTTTGGCAGATGCTTTAGTTACTACCAACCATGCCCTTTCCAGAGTACGGTCTACTTG 361
QY	361	ATGAATCTCTGGCTTTGGGATGTGCTGTGCAAGATGATTAATTTCCATTTGATTAAC 420
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Db	782	TGCTCCCGAGAGAGATCNGCACCCTCGGTAGGATCACCAGCTGCTCTGCTGGTGG 841
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Db	842	GTGGGCGAGTCTTTCGCTGCTGAGCT 867
RESULT 2		
LOCUS		CO960667
DEFINITION		AGENCOURT 30842630 NIH MGC_146 Homo sapiens cDNA clone
ACCESSION		IMAGE:7389810 5', mRNA sequence.
VERSION		CO960667
KEYWORDS		EST.
SOURCE		Homo sapiens (human)
ORGANISM		Homo sapiens
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS		1 (bases 1 to 762)
TITLE		NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL		National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT		Unpublished (1999)
		Contact: Daniela S. Gerhard, Ph.D.
		Office of Cancer Genomics
		National Cancer Institute / NIH
		Bldg. 31 Rm10A07 Bethesda, MD 20892
		Email: cgabs-remail.nih.gov
		Tissue Procurement: Guthrie cDNA Resource Center
		cDNA Library Preparation: Guthrie cDNA Resource Center
		cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
		DNA Sequencing by: Agencourt Bioscience Corporation
		Clone Distribution: MGC clone distribution information can be
		found through the I.M.A.G.E. Consortium/LLNL at:
		http://image.llnl.gov
		Plate: IRB78 row: d column: 04
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	/note="Vector: pCDNA3.1; Site 1: multiple; Site 2: multiple; ORF's were PCR-amplified (from IMAGE Clones or from commercially available cDNA libraries) and cloned by the Guthrie cDNA Resource Center (www.guthrie.org/cDNA) into pCDNA3.1. For specific information on cloning sites (which vary by clone), please refer to the Guthrie website, using the Guthrie ID given in the file ftp://image.llnl.gov/image/rearrayed_plates/IRBF.preSV.dat a. Note: this is a NIH_MGC library."	
ORIGIN	Query Match	50.4%; Score 581.8; DB 7; Length 762;
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	Matches	603; Conservative 0; Mismatches 17; Indels 1; Gaps 1;
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QY	61	TGCTGCCCCCACAAGCAGCGCTGGTTCCCGCTGGCGGAGCCCGACAGCAACGCG 120
Db	87	TGCTGCCCCCACAAGCAGCGCTGGTTCCCGCTGGCGGAGCCCGACAGCAACGCG 146
QY	121	AGCGCGGCTCGGAGGACGCGAGCTGGAGCCCGCGCACATCTCCCGGCCATCCCGGTC 180
Db	147	AGCGCGGCTCGGAGGACGCGAGCTGGAGCCCGCGCACATCTCCCGGCCATCCCGGTC 206
QY	181	ATCATCAAGCGGCTTACTCCGAGTGTTCGTCGTCGGCTGGTGGCAACTCGCTGGTC 240
Db	207	ATCATCAAGCGGCTTACTCCGAGTGTTCGTCGTCGGCTGGTGGCAACTCGCTGGTC 266
QY	241	ATGTTCTGTATCTCCGATACCAAGATGAAGACAGCAACCAATTACATATTAAAC 300
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Db	327	CTGGCTTTGGCAGATGCTTTAGTTACTACCAACCATGCCCTTTCCAGAGTACGGTCTACTTG 386
QY	361	ATGAATCTCTGGCTTTGGGATGTGCTGTGCAAGATGATTAATTTCCATTTGATTAAC 420

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 Qy 541 TGCACTCTGGCT-GCTGTGCTCATCTGTTGGGATCTCTGCAATAGTCCCTTGGAGGCCACCA 599  
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RESULT 3  
 CO960682/c  
 LOCUS  
 DEFINITION AGENCOURT 30842262 NIH MGC 146 Homo sapiens cDNA clone  
 IMAGE:7385610 3', mRNA sequence.

ACCESSION CO960682.1 GI:51325238

VERSION EST.

KEYWORDS Homo sapiens (human)

SOURCE EST.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TITLE NIH-MGC http://mgi.nci.nih.gov/.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Guthrie cDNA Resource Center

cDNA Library Preparation: Guthrie cDNA Resource Center

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: IRB18 row: d column: 04

High quality sequence start: 214

High quality sequence stop: 494.

Location/Qualifiers

1. .784

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/mol\_type="mRNA"

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/note="vector: pCDNA3.1; Site 1: multiple; Site 2:

multiple; ORF's were PCR-amplified (from IMAGE clones or

from commercially available cDNA libraries) and cloned by

the Guthrie cDNA Resource Center (www.guthrie.org/cDNA)

into pCDNA3.1. For specific information on cloning sites

(which vary by clone), please refer to the Guthrie

website, using the Guthrie ID given in the file

ftp://image.llnl.gov/image.rearrayed\_plates/IRBF.presv.dat

a. Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 45.0%; Score 518.8; DB 7; Length 784;

Best Local Similarity 97.6%; Pred. No. 5.3e-125;

Matches 537; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

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 Qy 646 GATGATGACTACTCTCTGGTGGGACCTCTTCAATGAAGATCTCGGTCTTCATCTTTGCCCTTC 705  
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 Qy 706 GTGATCCCTGTCCTCATCATCATCTGCTGTACACCCCTGATGATGATCCCTGCTCAAGAGC 765  
 Db 458 GTGATCCCTGTCCTCATCATCATCTGCTGTACACCCCTGATGATGATCCCTGCTCAAGAGC 399  
 Qy 766 GTCCGGCTCCTTTCTGGCTCCCGAGAGAAAGATCGCAACCTGCTAGGATCACCAGACTG 825  
 Db 398 GTCCGGCTCCTTTCTGGCTCCCGAGAGAAAGATCGCAACCTGCTAGGATCACCAGACTG 339  
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 Db 338 GTCTGTGTGTGGGAGCTTCTGCTGTCTGTGGAGCTCCCATTCACATTCATTCCTG 279  
 Qy 886 GTGGAGGCTCTGGGGAGCACCCTCCACAGACAGCTGCTCTCCAGTATTTACTTCTGC 945  
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 Qy 1006 AACTTCAAGCGTGTTCGGGAGCTTCTGCTTTCCACTCAAGATGAGGATGGAGCGGAG 1065  
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 Qy 1066 AGCACTAGCAGAGTCCGAATACAGTTCAGATCTCTTACCTGAGGAGCATCGATGGG 1125  
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 Qy 1126 ATGAATTAAC 1135  
 Db 38 ATGATGAAC 29

RESULT 4

CF593603

LOCUS

DEFINITION AGENCOURT 15623822 NIH MGC\_147 Homo sapiens cDNA clone

IMAGE:30531690 5', mRNA sequence.

ACCESSION CF593603

VERSION CF593603.1 GI:36347316

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 837)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Stefan Hanson

cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help

and advice from Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: NDAMG22 row: n column: 19

High quality sequence stop: 592.

**FEATURES**

1. .837

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1. 837
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insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
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preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: This is
a NIH MGC library."

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## ORIGIN

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Qy	121	AGCGCCGGCTCGGAGGACGGCAGCTGGAGCGCGCGCACATCTCTCCCGGCGCATCCCGGCT	180	
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LOCUS			
DEFINITION	Soares placenta Nb2HP Homo sapiens cDNA clone		
	IMAGE:998B19190 ; IMAGE:134322, mRNA sequence.		
ACCESSION	BX092912		
VERSION	BX092912.1		
KEYWORDS	GI:27823005		
SOURCE	EST.		
ORGANISM	Homo sapiens (human)		
	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 480)		
AUTHORS	Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,		
	Radelof, U., Schneider, D. and Korn, B.		
TITLE	Human Unigeneset - RZPD3		



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Qy 572 TCTCTGCAATAGTCTTGGAGGACCAAGTGCAGGAGAGCGTGCATGTCAATGAGTGTCT 631
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RESULT 7
AK043873
LOCUS
DEFINITION
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RECEPTOR, full insert sequence.
ACCESSION
AK043873.1 GI:26335979
VERSION
HTC; CAP trapper.
KEYWORDS
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
2 9279253
MEDLINE
10349636
PUBMED
10349636
AUTHORS
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL
20499374
MEDLINE
11042159
PUBMED
11042159
AUTHORS
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kiteunai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yamamoto,K., Matsumoto,H., Sakaguchi,S., Ikegami,I., Kashiwagi,K.,
Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
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```

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TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 4022)
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
Hori,F., Imotani,K., Iehii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
Kato,H., Kawai,O., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-resgsc.riken.jp,
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/
FEATURES
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sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

20530913

11076861

4

The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection

## Nature 4

25

The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

**Nature 420, 563-573 (2002)**

6 (bases 1 to 2959)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiroaka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tegami, M., Tagawa, A., Takahashi, F., Takaku-Akaira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

## Direct Submission

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cdna library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL:<http://genome.qsc.riken.jp/>

URL:<http://fantom.gsc.riken.jp/>.

## FEATURES

**source**

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DB	341	GCCTTCTGCCCCCTTGACCTCAAGGTACCATCGTGGGCTCTACTTGGCTGTGTGCATC	400	
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QY	334	ATGCCCTTTTCAGATGACGGTCTACTTTGATGAATTCCTTGGCTTTTGGGGATGTCCTGTC	393	
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JOURNAL REFERENCE	Nature 409, 685-690 (2001)
AUTHORS	5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL REFERENCE	Nature 420, 563-573 (2002)
AUTHORS	6 (bases 1 to 2940)
	Adachi, J., Aizawa, K., Anikura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanaoka, T., Hara, A., Hoshizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imokani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurahara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, K., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE	Direct Submission
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/ Location/Qualifiers
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DEFINITION	Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730079L19 product:NOICEPTIN RECEPTOR (ORPHANIN FQ RECEPTOR), full insert sequence.
ACCESSION	AK043275
VERSION	AK043275.1 GI:26089596
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
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TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalisation and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
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3
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Katsunai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2974)
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
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Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
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 (ORPHANIN FQ RECEPTOR), full insert sequence.

ACCESSION  
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 Mus musculus (house mouse)  
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 Mus musculus  
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
 1  
 Carninci,P. and Hayashizaki,Y.  
 TITLE  
 High-efficiency full-length cDNA cloning  
 JOURNAL  
 Meth. Enzymol. 303, 19-44 (1999)  
 MEDLINE  
 99279253  
 PUBMED  
 10349636

REFERENCE  
 2  
 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,  
 Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
 TITLE  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes  
 JOURNAL  
 Genome Res. 10 (10), 1617-1630 (2000)  
 MEDLINE  
 20499374  
 PUBMED  
 11042159

REFERENCE  
 3  
 Shibata,K., Itoh,M., Aizawa,K., Nagaoaka,S., Sasaki,N., Carninci,P.,  
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 Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
 TITLE  
 RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multipipette sequencer  
 JOURNAL  
 Genome Res. 10 (11), 1757-1771 (2000)  
 MEDLINE  
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 PUBMED  
 11076861

REFERENCE  
 4  
 The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 TITLE  
 Functional annotation of a full-length mouse cDNA collection  
 JOURNAL  
 Nature 409, 685-690 (2001)  
 MEDLINE  
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REFERENCE  
 5  
 The FANTOM Consortium and the RIKEN Genome Exploration Research  
 Group Phase I & II Team.  
 TITLE  
 Analysis of the mouse transcriptome based on functional annotation  
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 JOURNAL  
 Nature 420, 563-573 (2002)  
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REFERENCE  
 6  
 (bases 1 to 3101)  
 Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,  
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 Muramatsu,M. and Hayashizaki,Y.  
 TITLE  
 Direct Submission  
 JOURNAL  
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome

COMMENT  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
 Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,  
 URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,  
 Fax:81-45-503-9216)  
 cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Please visit our web site for further details.  
 URL:http://genome.gsc.riken.jp/  
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,  
1 (bases 1 to 879)  
Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,  
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,  
Adams, M.D. and Cargill, M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 879)  
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,  
Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B.,  
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,  
Adams, M.D. and Cargill, M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
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Matches 533; Conservative 0; Mismatches 297; Indels 9; Gaps 2;

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REFERENCE 1

**AUTHORS**  
 Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,  
 Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,P.,  
 Saurin,W. and Weissenbach,J.  
**TITLE**  
 Estimate of human gene number provided by genome-wide analysis  
 using Tetraodon nigroviridis DNA sequence  
**JOURNAL**  
 Nat. Genet. 25 (2), 235-238 (2000)  
**MEDLINE**  
 20296633  
**PUBMED**  
 10835645

**REFERENCE**  
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**AUTHORS**  
 Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,  
 Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,  
 Saurin,W., Bernot,A. and Weissenbach,J.  
**TITLE**  
 Characterization and repeat analysis of the compact genome of the  
 freshwater pufferfish tetraodon nigroviridis  
**JOURNAL**  
 Genome Res. 10 (7), 939-949 (2000)  
**MEDLINE**  
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**REFERENCE**  
 3 (bases 1 to 1053)

**AUTHORS**  
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 Direct Submission  
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 Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :  
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AUTHORS Zhu,J., Chen,C., Xue,J.-C., Kunapuli,S., Dierel,J.K. and  
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TITLE Cloning of a human kappa opioid receptor from the brain  
JOURNAL Life Sci. 56, 201-207 (1995)  
COMMENT Original source text: Homo sapiens (clone d2-115) (tissue library:  
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## ORIGIN

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 Unclassified.  
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 AUTHORS Au-Young, J. and Seilhamer, J.J.  
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 254 ATGTTGCTGATCATCCGATACACAAAGATGAAGACAGCAACCAATTTACATATTAAC 313  
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 374 ATGAATTCCTGCGCTTTGGGATGCTGTGCAAGATAGTAATTTCCATTTGATTAATAC 433  
 421 AACATGTTCCACAGCATCTTCCACCTTGACCATGATGAGCGTGGACCGCTACATTTGCGGTG 480  
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 661 TGGTGGGACCTCTTCAATGAAGATCTGCGTCTTTCATCTTTGCGCTTCGTGATCCCTGCTC 720  
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Db 1094 CGAATACAGTTCAGGATCCTGCTTACCTGAGGACATCGATGGATGAATAAACCCAGTA 1153  
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Db 1154 TGACTAGTCGTGGA 1167

RESULT 5  
AX548862  
LOCUS AX548862 1182 bp DNA linear PAT 26-NOV-2002  
DEFINITION Sequence 147 from Patent WO02061087.  
ACCESSION AX548862  
VERSION AX548862.1 GI:25813740  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE  
AUTHORS Burmer, G.C., Roush, C.L. and Brown, J.P.  
TITLE Antigenic peptides, such as for G protein-coupled receptors (GPCRs), antibodies thereto, and systems for identifying such antigenic peptides  
JOURNAL Patent: WO 02061087-A 147 08-AUG-2002;  
Lifespan Biosciences, Inc. (US)  
FEATURES  
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Query Match 99.2%; Score 1144.4; DB 6; Length 1182;  
Best Local Similarity 99.5%; Pred. No. 8.9e-201;  
Matches 1148; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGACTCCCGATCCAGATCTTCGGGGGAGCGGGCCCTACTGCGGCCCGCCAGCGCC 60  
Db 14 ATGGAATCCCGATTCAGATCTTCGGGGGAGCGCTGCGCCCTACTGCGGCCCGCCAGCGCC 73  
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Qy 121 AGCGCCCGCTCGAGGAGCGCGAGCTGCGAGCGCGCACATCTCCCGGCCATCCCGGTC 180  
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Qy 421 AACATGTTCCACGATCTTACCTTGACCATGATGAGCGGTGACCGCTACATTCGGGTG 480  
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Qy 781 GGCTCCCGAGAGAAGATCGCAACTGCTAGGATCACAGACTGGTCTCTGTTGGTGTG 840  
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Db 854 GCGGTTTTGCTGCTGCTGCACTCCCATTCACATATTCATCTCTGTTGGAGGCTCTGGG 913  
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Qy 1141 TGACTAGTCGTGGA 1154  
Db 1154 TGACTAGTCGTGGA 1167

RESULT 6  
AX774764  
LOCUS AX774764 1182 bp DNA linear PAT 09-JUL-2003  
DEFINITION Sequence 80 from Patent WO03038129.  
ACCESSION AX774764  
VERSION AX774764.1 GI:32486280  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE  
AUTHORS Raponi, M.  
TITLE Methods for assessing and treating leukemia  
JOURNAL Patent: WO 03038129-A 80 08-MAY-2003;  
Ortho-Clinical Diagnostics, Inc. (US)  
FEATURES  
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1. .1182  
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ORIGIN  
Query Match 99.2%; Score 1144.4; DB 6; Length 1182;





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Db 254 ATGTTCTGTCATCCGATACACAAAGATGAAGACAGCAACCAATTTACATTTAAC 313  
Qy 301 CTGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCCCTTTTCAGAGTACGCTTACTTTG 360  
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Qy 361 ATGAATTCCTGGCCTTTTGGGATGTCGTGCAAGATAGTAATTTCAITGATTAATAC 420  
Db 374 ATGAATTCCTGGCCTTTTGGGATGTCGTGCAAGATAGTAATTTCAITGATTAATAC 433  
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Qy 1141 TGACTAGTCGTGA 1154  
Db 1154 TGACTAGTCGTGA 1167

RESULT 8  
AR281679 AR281679 1143 bp DNA linear PAT 10-APR-2003  
LOCUS  
DEFINITION Sequence 1 from patent US 6518480.

ACCESSION AR281679  
VERSION AR281679.1 GI:29717434  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 1143)  
TITLE Conklin,B.R.  
JOURNAL Selective target cell activation by expression of a G  
FEATURES protein-coupled receptor activated superiorly by synthetic ligand  
source Patent: US 6518480-A 1 11-FEB-2003;  
location/Qualifiers  
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Query Match 98.9%; Score 1141.4; DB 6; Length 1143;  
Best Local Similarity 99.9%; Pred. No. 3.2e-200;  
Matches 1142; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1141 TG 1142
RESULT 10
LOCUS AR141371 1142 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 1 from patent US 6146835.
ACCESSION AR141371
VERSION AR141371.1 GI:15100887
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 1142)
AUTHORS Kieffer, B. and Simonin, F.
TITLE Human kappa opioid receptor, nucleic acids and uses thereof
JOURNAL Patent: US 6146835-A 1 14-NOV-2000;
FEATURES
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    Location/Qualifiers
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  Best Local Similarity 99.9%; Pred. No. 4.9e-200;
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ORIGIN									
Query Match 98.6%; Score 1138.2; DB 9; Length 1143; Best Local Similarity 99.7%; Pred. No. 1.2e-199; Matches 1140; Conservative 0; Mismatches 3; Indels 0; Gaps 0;									
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QY	61	TGCTTCCCGCCCAACAGACGCGCTGGTTTCCGCGTGGCGCGAGCCCGACAGCAACGCG	120						
DB	61	TGCTTCCCGCCCAACAGACGCGCTGGTTTCCGCGTGGCGCGAGCCCGACAGCAACGCG	120						
QY	121	AGCGCCGGCTCGGAGGACGCGAGCTGGAGCGCGGCACATCTCCCGCGCCATCCCGGTC	180						
DB	121	AGCGCCGGCTCGGAGGACGCGAGCTGGAGCGCGGCACATCTCCCGCGCCATCCCGGTC	180						
QY	181	ATCATCAGCGCGTCTACTCCGTAGTGTTCGTGCGGGCTTGGTGGGCAACTCGCTGGTC	240						
DB	181	ATCATCAGCGCGTCTACTCCGTAGTGTTCGTGCGGGCTTGGTGGGCAACTCGCTGGTC	240						
QY	241	ATGTTCTGTGATCATCCGATACCAAGATGAAGACAGCAACCAATTTACATATTAAAC	300						
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QY	301	CTGGCTTTGGCAGATGCTTTAGTTACTACCAACCATGCCCTTTACAGATGCGGTCTACTTG	360						
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QY	361	ATGAATCTCTGGCTTTGGGGATGCTGTGCAAGATAGTAATTTCCATTTGATTAATAC	420						
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QY	421	AACATGTTACACAGCATCTTCACTTGACCATGATGAGCGTGACCGCTACATTTGCCGTG	480						
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QY	481	TGCCACCCCGTGAAGGCTTTGGATCTCCGACACACCTTTGAAGCAAGATCATCAATATC	540						
DB	481	TGCCACCCCGTGAAGGCTTTGGATCTCCGACACACCTTTGAAGCAAGATCATCAATATC	540						
QY	541	TGCATCTGGCTGCTGCTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGACACAA	600						
DB	541	TGCATCTGGCTGCTGCTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGACACAA	600						
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DB	601	GTCAAGGAAGACGTCGATGTCAITGAGTGTCTTGCAGTTCCTGAGATGATGACTATCC	660						
QY	661	TGGTGGGACCTCTTCATGAAGATCTGGTCTTCACTTTGGCTTGGTATCCCTGTCCTC	720						
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DB	781	GGCTCCCGAGAGAAGATCGCAACCTCGTAGGATACCAAGATGCTGGTGGTGGTG	840						
QY	841	GCAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	900						
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QY	901	AGCACCTCCACAGCAGACGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT	960						
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DEFINITION AR281680									
ACCESSION AR281680									
VERSION AR281680.1 GI:29717435									
KEYWORDS									
SOURCE Unknown.									
ORGANISM Unclassified.									
REFERENCE 1 (bases 1 to 1284)									
AUTHORS Conklin,B.R.									
TITLE Selective target cell activation by expression of a G									
JOURNAL Protein-coupled receptor activated superiorly by synthetic ligand									
FEATURES Patent: US 6518480-A 3 11-FEB-2003;									
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DB	413	TGGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCCCTTTCAGAGTACGGTCT	472						
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
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JOURNAL				
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Arena Pharmaceuticals, Inc. (US)				
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 Lu, L.D. and Mansson, E.  
 Direct Submission  
 Submitted (23-OCT-2002) Molecular Biology, Adolor Corporation, 371  
 Phoenixville Pike, Malvern, PA 19355, USA  
 JOURNAL Location/Qualifiers  
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 ACCESSION AR281681  
 VERSION AR281681.1 GI:29717436  
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 ORGANISM Unknown.  
 REFERENCE Unclassified.  
 1 (bases 1 to 1275)  
 AUTHORS Conklin,B.R.  
 TITLE Selective target cell activation by expression of a G protein-coupled receptor activated superiorly by synthetic ligand

JOURNAL Patent: US 6518480-A 5 11-FEB-2003;

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Location/Qualifiers  
1. .1275  
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GenCore version 5.1.6  
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Listing first 45 summaries

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- 13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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6	1150.8	99.7	1154	12	ADN30507 Human kap
7	1150.8	99.7	1154	12	ADN30511 Human kap
8	1150.8	99.7	1154	12	ADN30509 Human kap
9	1144.4	99.2	1182	8	AB242678 Human opi
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14	1141.4	98.9	1143	2	AAT90998 Human kap
15	1140.4	98.8	1142	2	AAT12550 Human kap
16	1136.2	98.5	1284	2	AAT90999 Human kap
17	1136.2	98.5	1284	11	ADL90106 cDNA enco
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## ALIGNMENTS

### RESULT 1

ADN30508

ID ADN30508 standard; cDNA; 1154 BP.

XX AC ADN30508;

XX DT 12-AUG-2004 (first entry)

XX DE Human kappa opioid receptor, hKOR, C1008T allele.

XX KW Human; kappa opioid receptor; hKOR; ss; gene; SNP;  
 KW single nucleotide polymorphism; endogenous opioid system; nociception;  
 KW neurotransmitter release; learning; memory; cognition; pain; cocaine;  
 KW amphetamine; alcohol; tobacco; opiate; withdrawal;  
 KW neuroendocrine function; reproductive function; prolactin regulation;  
 KW stress responsiveness; mood; affect; immune function;  
 KW gastrointestinal function; analgesia; addictive disease;  
 KW chromosome 8q11.2.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
 XX allele replace(1008,C)  
 XX FT /\*tag= a

XX FT /standard\_name= "Single nucleotide polymorphism"

XX PN US2004097704-A1.

XX PD 20-MAY-2004.

XX PF 13-JUL-2001; 2001US-00904584.

XX PR 14-JUL-2000; 2000US-0218300P.

XX XX (KREEK/) KREEK M J.

XX PA (YUFE/) YUFEROV V.

XX PA (LAFO/) LAFORGE K S.

XX PI Kreek MJ, Yufarov V, Laforge KS;

XX XX WPI; 2004-389204/36.

XX PT Novel isolated variant allele of human kappa opioid receptor gene, useful

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variation /standard\_name= "Single nucleotide polymorphism"  
replace(948,T)  
/\*tag= e  
variation /standard\_name= "Single nucleotide polymorphism"  
replace(1008,T)  
/\*tag= f  
/standard\_name= "Single nucleotide polymorphism"

US2004097704-A1.

20-MAY-2004.

13-JUL-2001; 2001US-00904584.

14-JUL-2000; 2000US-0218300P.

(KREE/) KREEK M J.

(YUFE/) YUFEROV V.

(LAFO/) LAFORGE K S.

Kreek MJ, Yuferov V, Laforge KS;

WPI; 2004-389204/36.

Novel isolated variant allele of human kappa opioid receptor gene, useful for determining susceptibility in subject to physiological response, condition or disease related to endogenous opioid system.

Claim 1; SEQ ID NO 1; 29pp; English.

The invention relates to an isolated variant allele of a human kappa opioid receptor gene, comprising a DNA sequence having at least one variation in a fully defined wild-type allele of human kappa opioid receptor (hKOR) sequence appearing as ADN30505, where the variation comprises C852T, C948T, C1008T or their combinations. Also included are an isolated nucleic acid molecule selectively hybridizing to the variant, a cloning vector comprising the variant and an origin of replication, an expression vector comprising the variant associated with a promoter, a unicellular host transformed/transfected with the vector and a commercial test kit for determining the presence of at least one variation in a hKOR gene of an allele in a bodily sample taken from a subject. The hKOR variant allele is useful for determining a susceptibility in a subject to at least one physiological response, condition or disease related to the endogenous opioid system, nociception, neurotransmitter release, endogenous opioid system, learning, memory, cognition, pain, cocaine, amphetamine and other stimulants self-administration, behavioural sensitization to cocaine, opiates, alcohol and tobacco, opiate, amphetamine and alcohol withdrawal, physical dependence and tolerance, neuroendocrine function, reproductive function, prolactin regulation, stress responsiveness, physiology and pathology of mood and affect, immune function, gastrointestinal function. The hKOR variant allele is useful for determining a susceptibility to pain in a subject and is useful for determining a therapeutically effective amount of pain reliever to administer to a subject in order to induce analgesia in the subject. The hKOR variant allele is useful for determining a therapeutically effective amount of therapeutic agent to administer to a subject suffering from at least one addictive disease to treat the at least one addictive disease. The gene for hKOR is located on chromosome 8q11.2. The present sequence is the most common, wild-type allele of hKOR.

Sequence 1154 BP; 239 A; 339 C; 287 G; 289 T; 0 U; 0 Other;

Query Match

Best Local Similarity 99.9%; Score 1152.4; DB 12; Length 1154;

Pred. No. 2.4e-274;

	Matches 1153;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
Qy	1	ATGACTCCCGATCCAGATCTTCCGGGGGAGCGGSCCTTACTCGCCCGCCGAGCGCC	60						
Db	1	ATGACTCCCGATCCAGATCTTCCGGGGGAGCGGSCCTTACTCGCCCGCCGAGCGCC	60						
Qy	61	TGCTGCCCCCACAACAGCAGCGCTTGTTCCTCCGGCTGGGCGAGCCCGACAGCAACGGC	120						
Db	61	TGCTGCCCCCACAACAGCAGCGCTTGTTCCTCCGGCTGGGCGAGCCCGACAGCAACGGC	120						
Qy	121	AGCCCGGCTCGAGGAGCGCAGCTGAGAGCCCGGACACATCTCCCGGCGCATCCCGGTC	180						
Db	121	AGCCCGGCTCGAGGAGCGCAGCTGAGAGCCCGGACACATCTCCCGGCGCATCCCGGTC	180						
Qy	181	ATCATACGGGGTCTACTCCGTAGTGTTCGTCTGGGCTTGGTGGGCACTCGCTGGTC	240						
Db	181	ATCATACGGGGTCTACTCCGTAGTGTTCGTCTGGGCTTGGTGGGCACTCGCTGGTC	240						
Qy	241	ATGTTCTGTATCATCCGATACACAAAGATGAAGACAGCAACCAATTTACATATTTAAC	300						
Db	241	ATGTTCTGTATCATCCGATACACAAAGATGAAGACAGCAACCAATTTACATATTTAAC	300						
Qy	301	CTGCTTTGGCAGATGCTTTTAGTTACTACAACCATGCCCTTTTTCAGAGTACGGTCTACTG	360						
Db	301	CTGCTTTGGCAGATGCTTTTAGTTACTACAACCATGCCCTTTTTCAGAGTACGGTCTACTG	360						
Qy	361	ATGAATTCCTGGGCTTTTGGGATGCTGTGCAAGATAGTAATTTCCATTGATTACTAC	420						
Db	361	ATGAATTCCTGGGCTTTTGGGATGCTGTGCAAGATAGTAATTTCCATTGATTACTAC	420						
Qy	421	AACATGTTTCAACGATCTTTCACCTTGACCATGATGAGCGTGGACCGCTACATTTGCCGTG	480						
Db	421	AACATGTTTCAACGATCTTTCACCTTGACCATGATGAGCGTGGACCGCTACATTTGCCGTG	480						
Qy	481	TGCCACCCCGTGAAGGCTTTGGACTTCGACACACCTTTGAAGGCAAGATCATCAATATC	540						
Db	481	TGCCACCCCGTGAAGGCTTTGGACTTCGACACACCTTTGAAGGCAAGATCATCAATATC	540						
Qy	541	TGCATCTGGTGTCTGTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGACCAAA	600						
Db	541	TGCATCTGGTGTCTGTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGACCAAA	600						
Qy	601	GTGAGGAAGACGTCGATGTCATTGAGTGTCTTTCGAGTTCCTCCAGATGATGACTACTCC	660						
Db	601	GTGAGGAAGACGTCGATGTCATTGAGTGTCTTTCGAGTTCCTCCAGATGATGACTACTCC	660						
Qy	661	TGTTGGAGCTCTTCATGAAGATCTGGTCTTTCATCTTTGCTTTCGATGATCCCTGCTCTC	720						
Db	661	TGTTGGAGCTCTTCATGAAGATCTGGTCTTTCATCTTTGCTTTCGATGATCCCTGCTCTC	720						
Qy	721	ATCATCATCTCTGCTACACCTGATGATCTCGGTCTCAAGAGCGTCCGCTCTTCT	780						
Db	721	ATCATCATCTCTGCTACACCTGATGATCTCGGTCTCAAGAGCGTCCGCTCTTCT	780						
Qy	781	GGCTCCCGAGAGAAGATCGCAACCTCGTAGGATCACCAGACTGGTCTGGTGGTGGTG	840						
Db	781	GGCTCCCGAGAGAAGATCGCAACCTCGTAGGATCACCAGACTGGTCTGGTGGTGGTG	840						
Qy	841	GCAGTCTTCGTCTGCTGAGCTCCCATTCACATATTCATCTCGTGGAGGCTCTGGGG	900						
Db	841	GCAGTCTTCGTCTGCTGAGCTCCCATTCACATATTCATCTCGTGGAGGCTCTGGGG	900						
Qy	901	AGACCTCCACAGCAGCTGCTCTCCAGCTATTACTTCTGATGAAAAATTTCAACGGGTGT	960						
Db	901	AGACCTCCACAGCAGCTGCTCTCCAGCTATTACTTCTGATGAAAAATTTCAACGGGTGT	960						
Qy	961	ACCAACAGTAGTGAATCCCATTTCTAGCCCTTTCTTGTAGTAAAAATTTCAACGGGTGT	1020						
Db	961	ACCAACAGTAGTGAATCCCATTTCTAGCCCTTTCTTGTAGTAAAAATTTCAACGGGTGT	1020						
Qy	1021	TTCCGGGACTTCTGCTTTTCCACTGAAGATGAGGATGAGCGGCGCAGACACTAGCAGATC	1080						
Db	1021	TTCCGGGACTTCTGCTTTTCCACTGAAGATGAGGATGAGCGGCGCAGACACTAGCAGATC	1080						

QY 1081 CGAAATACAGTTCAGGATCCTGTTACCTGAGGACATCGATGGATGAATAAACAGTA 1140  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 1081 CGAAATACAGTTCAGGATCCTGTTACCTGAGGACATCGATGGATGAATAAACAGTA 1140  
 QY 1141 TGACTAGTCGTGGA 1154  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 1141 TGACTAGTCGTGGA 1154

RESULT 3  
 ID ADR44858  
 AD ADR44858 standard; cDNA; 1154 BP.  
 AC ADR44858;  
 DT 18-NOV-2004 (first entry)  
 XX Human kappa opioid receptor encoding cDNA SEQ ID NO:30.  
 DE  
 XX  
 KW opioid receptor; nerve cell; analgesic; gene therapy; pain; human;  
 KW kappa opioid receptor; chromosome 8; gene; ss.  
 OS Homo sapiens.  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT 1..1143  
 FT CDS /\*tag= a  
 FT /\*product= "kappa opioid receptor"

XX WO2004073646-A2.  
 PN  
 XX  
 PD 02-SEP-2004.  
 XX  
 PF 19-FEB-2004; 2004WO-US004914.  
 XX  
 PR 19-FEB-2003; 2003US-0448663P.  
 XX  
 XX (UYRP ) UNIV ROCHESTER.  
 XX  
 XX Kyrkanides S, Tallents RH;  
 FI  
 XX  
 XX  
 DR WPI; 2004-635472/61.  
 DR P-PSDB; ADR44857.  
 DR GENBANK; U17298.  
 XX

XX New vector for delivering an opioid receptor to a nerve cell comprising a  
 PT sequence encoding a mu-opioid receptor and a vector backbone, useful in  
 PT preparing a composition for reducing pain.  
 XX  
 XX Disclosure; SEQ ID NO 30; 147pp; English.  
 XX  
 CC The present invention describes a vector for delivering an opioid  
 CC receptor to a nerve cell. The method comprises a sequence encoding an  
 CC opioid receptor and a vector backbone. Also described: (1) a cell  
 CC comprising the vector or its integrated product; (2) an animal comprising  
 CC the cell; (3) reducing pain in a subject; (4) producing the vector; (5)  
 CC producing the cell; and (6) an animal produced by the process of  
 CC administering the vector to the animal. The vector has analgesic  
 CC activity, and can be used in gene therapy. The vector is useful in  
 CC preparing a composition for reducing pain in a subject. The present  
 CC sequence encodes the human kappa opioid receptor, which is used in the  
 CC exemplification of the present invention. The human kappa opioid receptor  
 CC gene is located on chromosome 8, more specifically to 8q11-12.  
 XX  
 XX Sequence 1154 BP; 239 A; 339 C; 287 G; 289 T; 0 U; 0 Other;

Query Match 99.9%; Score 1152.4; DB 13; Length 1154;  
 Best Local Similarity 99.9%; Pred. No. 2.4e-274;  
 Matches 1153; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 ATGGATCCCGATCCAGATCTTCGCGGGAGCGCGGCCCTTACCTGCGCCCGAGGGCC 60  
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DB 1 ATGGATCCCGATCCAGATCTTCGCGGGAGCGCGGCCCTTACCTGCGCCCGAGGGCC 60  
 QY 61 TCCCTGCCCGCCCAACAGAGAGCGCCTGGTTTCCCGCTGGGCGGAGCCCGACAGCAACGCG 120  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 61 TCCCTGCCCGCCCAACAGAGAGCGCCTGGTTTCCCGCTGGGCGGAGCCCGACAGCAACGCG 120  
 QY 121 AGCGCGGCTCGGAGGACGCGCAGCTGGAGCCCGGCGCACATCTCCCGGCCATCCCGGTC 180  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 121 AGCGCGGCTCGGAGGACGCGCAGCTGGAGCCCGGCGCACATCTCCCGGCCATCCCGGTC 180  
 QY 181 ATCATCAGCGGCTCTACTCGTAGTGTTCGTCGTGGGCTGGTGGGCACTCGCTGGTC 240  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 181 ATCATCAGCGGCTCTACTCGTAGTGTTCGTCGTGGGCTGGTGGGCACTCGCTGGTC 240  
 QY 241 ATGTTCTGTCATCCGATACACAAAGATGAAGACAGCAACCAACATTTTACATATTAAAC 300  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 241 ATGTTCTGTCATCCGATACACAAAGATGAAGACAGCAACCAACATTTTACATATTAAAC 300  
 QY 301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTTACAGAGTACGGTCTACTTG 360  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 301 CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTTACAGAGTACGGTCTACTTG 360  
 QY 361 ATGAATTCCTGGCCTTTTGGGATGTCGTGCAAGATAGTAATTTCCATTGATTACTAC 420  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 361 ATGAATTCCTGGCCTTTTGGGATGTCGTGCAAGATAGTAATTTCCATTGATTACTAC 420  
 QY 421 AACATGTTTCCAGCATCTTACCTTGACCATGATGAGGCGGTCGCTACATTTGCCGTC 480  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 421 AACATGTTTCCAGCATCTTACCTTGACCATGATGAGGCGGTCGCTACATTTGCCGTC 480  
 QY 481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCAACACCTTTGAAGGCAAGATCAATATTC 540  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 481 TGCCACCCCGTGAAGGCTTTGGACTTCCGCAACACCTTTGAAGGCAAGATCAATATTC 540  
 QY 541 TGCATCTGGCTGCTGTGTCATCTGTGGCATCTCTGCAATAGTCTTGGAGGCAACCA 600  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
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 QY 601 GTGAGGAAGCTCGATGTCATTTGAGTCTCTTGGAGTCCAGATGATGATGATCTCC 660  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 601 GTGAGGAAGCTCGATGTCATTTGAGTCTCTTGGAGTCCAGATGATGATGATCTCC 660  
 QY 661 TCGTGGGACCTTTTATGAAGATCTGCGTCTTTCATCTTTTGGCTTCTGTCGTCCTCT 720  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 661 TCGTGGGACCTTTTATGAAGATCTGCGTCTTTCATCTTTTGGCTTCTGTCGTCCTCT 720  
 QY 721 ATCATCATGTCGTGTACACCTGATGATCTCGGCTCTCAAGAGGCTCGGCTCCTTCT 780  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
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 QY 781 GGCTCCCGAGAGAAAGATCGCAACCTGCTAGGATCACCAGACTGGTCTGCTGGTGGTG 840  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 781 GGCTCCCGAGAGAAAGATCGCAACCTGCTAGGATCACCAGACTGGTCTGCTGGTGGTG 840  
 QY 841 GCAGTCTTCGTCTGTCGTGGACTCCCATTCATATTTTCATCTGCTGGTGGAGCTCTGG 900  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 841 GCAGTCTTCGTCTGTCGTGGACTCCCATTCATATTTTCATCTGCTGGTGGAGCTCTGG 900  
 QY 901 AGACCTCCACAGACAGCTGCTCTCCAGCTATTACTTCTGTCATCGCTTGGCTTAT 960  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 901 AGACCTCCACAGACAGCTGCTCTCCAGCTATTACTTCTGTCATCGCTTGGCTTAT 960  
 QY 961 ACCAAGTAGGCTGAATCCCATCTTCTACGCTTCTTGTGATGAAATTTCAAGCGGTGT 1020  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
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 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGAGACTAGCAGAGTC 1080  
 QY 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGACATCGATGGGATGAATAAACAGTA 1140  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 1081 CGAAATACAGTTCAGGATCCTGCTTACCTGAGGACATCGATGGGATGAATAAACAGTA 1140

QY 1141 TGACTAGTCGTGGA 1154  
 DB 1141 TGACTAGTCGTGGA 1154

RESULT 4  
 ADN30506  
 ID ADN30506 standard; cDNA; 1154 BP.  
 XX  
 AC ADN30506;  
 XX  
 DT 12-AUG-2004 (first entry)  
 XX  
 DE Human kappa opioid receptor, hKOR, C852T allele.  
 XX  
 KW Human; kappa opioid receptor; hKOR; ss; gene; SNP;  
 KW single nucleotide polymorphism; endogenous opioid system; nociception;  
 KW neurotransmitter release; learning; memory; cognition; pain; cocaine;  
 KW amphetamine; alcohol; tobacco; opiate; withdrawal;  
 KW neuroendocrine function; reproductive function; prolactin regulation;  
 KW stress responsivity; mood; affect; immune function;  
 KW gastrointestinal function; analgesia; addictive disease;  
 KW chromosome 8q11.2.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT allele replace(852,C)  
 FT /\*tag= a  
 FT /standard\_name= "single nucleotide polymorphism"  
 XX  
 PN US2004097704-A1.  
 XX  
 XX 20-MAY-2004.  
 XX  
 XX 13-JUL-2001; 2001US-00904584.  
 XX  
 XX 14-JUL-2000; 2000US-0218300P.  
 XX  
 XX (KREE/) KREEK M J.  
 XX (YUFE/) YUFEROV V.  
 XX (LAFO/) LAFORGE K S.  
 XX  
 XX Kreek MJ, Yufarov V, Laforge KS;  
 XX WPI; 2004-389204/36.  
 XX  
 XX Novel isolated variant allele of human kappa opioid receptor gene, useful  
 XX for determining susceptibility in subject to physiological response,  
 XX condition or disease related to endogenous opioid system.  
 XX  
 XX Example; SEQ ID NO 2; 29pp; English.  
 XX  
 XX The invention relates to an isolated variant allele of a human kappa  
 XX opioid receptor gene, comprising a DNA sequence having at least one  
 XX variation in a fully defined wild-type allele of human kappa opioid  
 XX receptor (hKOR) sequence appearing as ADN30505, where the variation  
 XX comprises C852T, C948T, C1008T or their combinations. Also included are  
 XX an isolated nucleic acid molecule selectively hybridising to the variant,  
 XX a cloning vector comprising the variant and an origin of replication, an  
 XX expression vector comprising the variant associated with a promoter, a  
 XX unicellular host transformed/transfected with the vector and a commercial  
 XX test kit for determining the presence of at least one variation in a hKOR  
 XX gene of an allele in a bodily sample taken from a subject. The hKOR  
 XX variant allele is useful for determining a susceptibility in a subject to  
 XX at least one physiological response, condition or disease related to the  
 XX endogenous opioid system, nociception, neurotransmitter release  
 XX endogenous opioid system, learning, memory, cognition, pain, cocaine,  
 XX amphetamine and other stimulants self-administration, behavioural  
 XX sensitisation to cocaine, opiates, alcohol and tobacco, opiate,  
 XX amphetamine and alcohol withdrawal, physical dependence and tolerance;  
 XX neuroendocrine function, reproductive function, prolactin regulation,

CC stress responsivity, physiology and pathology of mood and affect, immune  
 CC function, gastrointestinal function. The hKOR variant allele is useful  
 CC for determining a susceptibility to pain in a subject and is useful for  
 CC determining a therapeutically effective amount of pain reliever to  
 CC administer to a subject in order to induce analgesia in the subject. The  
 CC hKOR variant allele is useful for determining a therapeutically effective  
 CC amount of therapeutic agent to administer to a subject suffering from at  
 CC least one addictive disease to treat the at least one addictive disease.  
 CC The gene for hKOR is located on chromosome 8q11.2. The present sequence  
 CC is the C852T allele of hKOR.  
 XX  
 XX Sequence 1154 BP; 239 A; 338 C; 287 G; 290 T; 0 U; 0 Other;  
 XX  
 XX Query Match 99.7%; Score 1150.8; DB 12; Length 1154;  
 XX Best Local Similarity 99.8%; Pred. No. 5.9e-274;  
 XX Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 ATGGACTCCCGATCCAGATCTTCGCGGGGAGCGGGCCCTACTGGGCCCCGAGCGCC 60  
 DB 1 ATGGACTCCCGATCCAGATCTTCGCGGGGAGCGGGCCCTACTGGGCCCCGAGCGCC 60  
 QY 61 TGCCTGCCCGCCCAACACGACGCGCTGTTCCCGGCTGGGCGGAGCCGACGCAACGGC 120  
 DB 61 TGCCTGCCCGCCCAACACGACGCGCTGTTCCCGGCTGGGCGGAGCCGACGCAACGGC 120  
 QY 121 AGCGCCGGCTCGGAGGACGCGCAGCTGGAGCCCGCGCACATCTCCCGGGCCATCCCGGTC 180  
 DB 121 AGCGCCGGCTCGGAGGACGCGCAGCTGGAGCCCGCGCACATCTCCCGGGCCATCCCGGTC 180  
 QY 181 ATCATACGCGGGTCTACTCGTAGTGTTCGTCGGGCTGGTGGGCACTCGCTGGTC 240  
 DB 181 ATCATACGCGGGTCTACTCGTAGTGTTCGTCGGGCTGGTGGGCACTCGCTGGTC 240  
 QY 241 ATGTTCTGTGATCATCCGATACAAAGATGAAGACAGCAACCAATTTACATATTAAAC 300  
 DB 241 ATGTTCTGTGATCATCCGATACAAAGATGAAGACAGCAACCAATTTACATATTAAAC 300  
 QY 301 CTGGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCCCCTTTTCAGAGTACGGTCTACTTG 360  
 DB 301 CTGGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCCCCTTTTCAGAGTACGGTCTACTTG 360  
 QY 361 ATGAATTCCTGGGCTTTGGGGATGCTGTGCAAGATAGTAATTCATTTGATTAATAC 420  
 DB 361 ATGAATTCCTGGGCTTTGGGGATGCTGTGCAAGATAGTAATTCATTTGATTAATAC 420  
 QY 421 AACATGTTACCCAGCATCTTACCTTCAGCATGATGAGCGTGACCGCTACATTTGCCGTG 480  
 DB 421 AACATGTTACCCAGCATCTTACCTTCAGCATGATGAGCGTGACCGCTACATTTGCCGTG 480  
 QY 481 TGCCACCCCGTGAAGGCTTTGGGACTTCCGCACACCCCTTGAAGGCAAGATCATCAATATC 540  
 DB 481 TGCCACCCCGTGAAGGCTTTGGGACTTCCGCACACCCCTTGAAGGCAAGATCATCAATATC 540  
 QY 541 TGATCTGGCTGCTGTCGTATCTGTTGGCATCTCTGCAATAGTCTTTGGAGGACCAAA 600  
 DB 541 TGATCTGGCTGCTGTCGTATCTGTTGGCATCTCTGCAATAGTCTTTGGAGGACCAAA 600  
 QY 601 GTCAGGGAAGACGTCGATGTCATTGAGTGTCTTTCAGTTCCTCCAGATGATGACTACTCC 660  
 DB 601 GTCAGGGAAGACGTCGATGTCATTGAGTGTCTTTCAGTTCCTCCAGATGATGACTACTCC 660  
 QY 661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTTGCCTTCGTTGATCCCTGCTC 720  
 DB 661 TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTTGCCTTCGTTGATCCCTGCTC 720  
 QY 721 ATCATCATGCTGTGTACACCCCTGATGATCCTGGTCTCAAGAGCGTCCGGCTCTTCT 780  
 DB 721 ATCATCATGCTGTGTGTACACCCCTGATGATCCTGGTCTCAAGAGCGTCCGGCTCTTCT 780  
 QY 781 GGCTCCCGAGAGAAGATCCCAACCTGCGTAGATCACCAGACTGGTCTGGTGGTGGTG 840  
 DB 781 GGCTCCCGAGAGAAGATCCCAACCTGCGTAGATCACCAGACTGGTCTGGTGGTGGTG 840

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QY 841 GCAGCTTCGTCTGCTGGACTCCATTACATATTCATCTGCTGAGGCTCTGGGG 900
DB 841 GCAGCTTCGTCTGCTGGACTCCCATTCACATATTCATCTGCTGAGGCTCTGGGG 900
QY 901 AGCACCTCCACAGCAGACGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960
DB 901 AGCACCTCCACAGCAGACGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT 960
QY 961 ACCAACAGTAGCTGAATCCCATCTCTACGCTTCTTCTTGATGAAATTTCAAGCGGTGT 1020
DB 961 ACCAACAGTAGCTGAATCCCATCTCTACGCTTCTTCTTGATGAAATTTCAAGCGGTGT 1020
QY 1021 TTCGGGACTTCGCTTTCACCTGAGATGAGGATGGAGCGGACAGACTAGCAGAGTC 1080
DB 1021 TTCGGGACTTCGCTTTCACCTGAGATGAGGATGGAGCGGACAGACTAGCAGAGTC 1080
QY 1081 CGAAATACAGTTTCAGGATCTGCTTACCTGAGGACATCGATGGGATGAATAAACAGTA 1140
DB 1081 CGAAATACAGTTTCAGGATCTGCTTACCTGAGGACATCGATGGGATGAATAAACAGTA 1140
QY 1141 TGACTAGTCGTGGA 1154
DB 1141 TGACTAGTCGTGGA 1154

RESULT 5
ADN30510
ID ADN30510 standard; cDNA; 1154 BP.
XX
XX ADN30510;
XX
XX 12-AUG-2004 (first entry)
XX
XX Human kappa opioid receptor, hKOR, A843G allele.
XX
XX Human; kappa opioid receptor; hKOR; ss; gene; SNP;
XX single nucleotide polymorphism; endogenous opioid system; nociception;
XX neurotransmitter release; learning; memory; cognition; pain; cocaine;
XX amphetamine; alcohol; tobacco; opiate; withdrawal;
XX neuroendocrine function; reproductive function; prolactin regulation;
XX stress responsivity; mood; affect; immune function;
XX gastrointestinal function; analgesia; addictive disease;
XX chromosome 8q11.2.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX allele /*tag= a
XX /standard_name= "Single nucleotide polymorphism"
XX
XX US2004097704-A1.
XX
XX 20-MAY-2004.
XX
XX 13-JUL-2001; 2001US-00904584.
XX
XX 14-JUL-2000; 2000US-0218300P.
XX
XX (KREE/) KREEK M J.
XX (YUFE/) YUFEROV V.
XX (LAFO/) LAFORGE K S.
XX
XX Kreek MJ, Yuferov V, Laforge KS;
XX WPI; 2004-389204/36.
XX
XX Novel isolated variant allele of human kappa opioid receptor gene, useful
XX for determining susceptibility in subject to physiological response,
XX condition or disease related to endogenous opioid system.
XX
XX Example; SEQ ID NO 6; 29pp; English.
XX
```

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CC The invention relates to an isolated variant allele of a human kappa
CC opioid receptor gene, comprising a DNA sequence having at least one
CC variation in a fully defined wild-type allele of human kappa opioid
CC receptor (hKOR) sequence appearing as ADN30505, where the variation
CC comprises C852T, C948T, C1008T or their combinations. Also included are
CC an isolated nucleic acid molecule selectively hybridising to the variant,
CC a cloning vector comprising the variant and an origin of replication, an
CC expression vector comprising the variant associated with a promoter, a
CC unicellular host transformed/transfected with the vector and a commercial
CC test kit for determining the presence of at least one variation in a hKOR
CC gene of an allele in a bodily sample taken from a subject. The hKOR
CC variant allele is useful for determining a susceptibility in a subject to
CC at least one physiological response, condition or disease related to the
CC endogenous opioid system, nociception, neurotransmitter release
CC amphetamine and other stimulants self-administration, behavioural
CC sensitisation to cocaine, opiates, alcohol and tobacco, opiate,
CC amphetamine and alcohol withdrawal, physical dependence and tolerance;
CC neuroendocrine function, reproductive function, prolactin regulation,
CC stress responsivity, physiology and pathology of mood and affect, immune
CC function, gastrointestinal function. The hKOR variant allele is useful
CC for determining a susceptibility to pain in a subject and is useful for
CC determining a therapeutically effective amount of pain reliever to
CC administer to a subject in order to induce analgesia in the subject. The
CC hKOR variant allele is useful for determining a therapeutically effective
CC amount of therapeutic agent to administer to a subject suffering from at
CC least one addictive disease to treat the at least one addictive disease.
CC The gene for hKOR is located on chromosome 8q11.2. The present sequence
CC is the A843G allele of hKOR.
XX
XX SQ Sequence 1154 BP; 238 A; 339 C; 288 G; 289 T; 0 U; 0 Other;
```

```
Query Match 99.7%; Score 1150.8; DB 12; Length 1154;
Best Local Similarity 99.8%; Pred. No. 5.9e-274;
Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGGACTCTCCCGATCCAGATCTTCCGCGGGAGCGGGCCCTTACTTGGCCGCCGAGCGCC 60
DB 1 ATGGACTCTCCCGATCCAGATCTTCCGCGGGAGCGGGCCCTTACTTGGCCGCCGAGCGCC 60
QY 61 TGCCTGCCGCCCAACAGCAGCGCCCTTGGTTCCCGGCTGGCGGCGGAGCCGACGACGACGCG 120
DB 61 TGCCTGCCGCCCAACAGCAGCGCCCTTGGTTCCCGGCTGGCGGCGGAGCCGACGACGACGCG 120
QY 121 AGCGCGGCTCGGAGGAGCGCGAGCTGGAGCGCGGCGCACATCTCCCGCGGCCATCCCGGTC 180
DB 121 AGCGCGGCTCGGAGGAGCGCGAGCTGGAGCGCGGCGCACATCTCCCGCGGCCATCCCGGTC 180
QY 181 ATCATCAGCGGCTTACTTCCGTAGTGTTCGTGGGGCTTGGTGGGCGAATCGCTGGTC 240
DB 181 ATCATCAGCGGCTTACTTCCGTAGTGTTCGTGGGGCTTGGTGGGCGAATCGCTGGTC 240
QY 241 ATGTTCTGTGATCATCCGATACACAAAGATGAGAGCAGCAACCAATTTTACATATTAAAC 300
DB 241 ATGTTCTGTGATCATCCGATACACAAAGATGAGAGCAGCAACCAATTTTACATATTAAAC 300
QY 301 CTGGCTTTTGGCAGATGCTTTAGTTACTACAAACATGCGCCCTTTTCCAGAGTACGGTCTT 360
DB 301 CTGGCTTTTGGCAGATGCTTTAGTTACTACAAACATGCGCCCTTTTCCAGAGTACGGTCTT 360
QY 361 ATGAATTCCTGGCCTTTTGGGATGCTGTGTCGAGATAGTAAATTTCCATTGATTACTAC 420
DB 361 ATGAATTCCTGGCCTTTTGGGATGCTGTGTCGAGATAGTAAATTTCCATTGATTACTAC 420
QY 421 AACATGTTTCCAGCAGATCTTCCACCTTGACCATGATGAGCGTGACCGCTACATTGGCGTG 480
DB 421 AACATGTTTCCAGCAGATCTTCCACCTTGACCATGATGAGCGTGACCGCTACATTGGCGTG 480
QY 481 TGCCACCCCGCTGAAGGCTTTTGGACTTTCGACACACCCCTTGAAGGCAAGATCATCAATATC 540
DB 481 TGCCACCCCGCTGAAGGCTTTTGGACTTTCGACACACCCCTTGAAGGCAAGATCATCAATATC 540
QY 541 TGCATCTGGCTGCTGTCGTCATCTGTGGCATCTCTGCAATAGTCTCTGGAGGACCACAA 600
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[illegible]

RESULT 6  
ADN30507  
ID ADN30507 standard; cDNA; 1154 BP.  
XX  
AC ADN30507;

DT 12-AUG-2004 (first entry)

XX Human kappa opioid receptor, hKOR, C948T allele.

Human; kappa opioid receptor; hKOR; ss; gene; SNP;  
 single nucleotide polymorphism; endogenous opioid system; nociception;  
 neurotransmitter release; learning; memory; cognition; pain; cocaine;  
 amphetamine; alcohol; tobacco; opiate; withdrawal;  
 neuroendocrine function; reproductive function; prolactin regulation;  
 stress responsiveness; mood; affect; immune function;  
 gastrointestinal function; analgesia; additive disease;  
 chromosome 8q11.2.

OS Homo sapiens.

XX	Key	Location/Qualifiers
FH	allele	replace (948,C)
FT		

```
ET      / *tag= a
ET      /standard name= "Single nucleotide polymorphism"
```

XX PN US2004097704-A1.

20-MAY-2004.  
PD  
XX

XX	13-JUL-2001; 2001US-00904584.
PF	
XX	
XX	14-JUL-2000; 2000US-0218300P.
PR	
XX	
XX	(KREE/) KREEK M J.
PA	(YUFE/) YUFEROV V.
PA	(LAFO/) LAFORGE K S.
PA	
XX	Kreek MJ, Yuferov V, Laforge
PI	
XX	WPI; 2004-389204/36.
XX	
DR	

PT Novel isolated variant allele of human kappa opioid receptor gene, useful for determining susceptibility in subject to physiological response, PT condition or disease related to endogenous opioid system.

PS Example; SEQ ID NO 3; 29pp; English.

The invention relates to an isolated variant allele of a human kappa opioid receptor gene, comprising a DNA sequence having at least one variation in a fully defined wild-type allele of human kappa opioid receptor (hKOR) sequence appearing as ADN30505, where the variation comprises C852T, C948T, C1008T or their combinations. Also included are an isolated nucleic acid molecule selectively hybridising to the variant, a cloning vector comprising the variant and an origin of replication, an expression vector comprising the variant associated with a promoter, a unicellular host transformed/transfected with the vector and a commercial test kit for determining the presence of at least one variation in a hKOR gene of an allele in a bodily sample taken from a subject. The hKOR variant allele is useful for determining a susceptibility in a subject to at least one physiological response, condition or disease related to the endogenous opioid system, nociception, neurotransmitter release endogenous opioid system, learning, memory, cognition, pain, cocaine, amphetamine and other stimulants self-administration, behavioural sensitisation to cocaine, opiates, alcohol and tobacco, opiate, amphetamine and alcohol withdrawal, physical dependence and tolerance; neuroendocrine function, reproductive function, prolactin regulation, stress responsiveness, physiology and pathology of mood and affect, immune function, gastrointestinal function. The hKOR variant allele is useful for determining a susceptibility to pain in a subject and is useful for determining a therapeutically effective amount of pain reliever to administer to a subject in order to induce analgesia in the subject. The hKOR variant allele is useful for determining a therapeutically effective amount of therapeutic agent to administer to a subject suffering from at least one addictive disease to treat the at least one addictive disease. The gene for hKOR is located on chromosome 8q11.2. The present sequence is the C948T allele of hKOR.

Sequence 1154 BP; 239 A; 338 C; 287 G; 290 T; 0 U; 0 Other;

Query Match	99.7%	Score 1150.8	DB 12	Length 1154
Best Local Similarity	99.8%	Pred. No. 5.9e-274		
Matches 1152	Conservative 0	Mismatches 2	Indels 0	Gaps 0
Qy	1	ATGGACTCCCGCATCCAGATCTTCGGGGGAGCGCGGGCCCTACCTCGCGCCCGCAGCGCC	60	
Db	1	ATGGACTCCCGCATCCAGATCTTCGGGGGAGCGCGGGCCCTACCTCGCGCCCGCAGCGCC	60	
Qy	61	TGCGTCGCCGCCCAACAGCAGCGCGCTGGTTTTCGCGGCTGGGCGCAGCCGACGAAACGGC	120	
Db	61	TGCGTCGCCGCCCAACAGCAGCGCGCTGGTTTTCGCGGCTGGGCGCAGCCGACGAAACGGC	120	
Qy	121	AGCGCGGCTCGAGGACGGCGAGCTGGAGCGCGCGCACATCTCCCGGCCATCCCGGTC	180	
Db	121	AGCGCGGCTCGAGGACGGCGAGCTGGAGCGCGCGCACATCTCCCGGCCATCCCGGTC	180	
Qy	181	ATCATCACGGCGGTCTACTCCGTAGTGTCTCGTGTGGGCTTGGTGGGCAACTCGCTGGTC	240	
Db	181	ATCATCACGGCGGTCTACTCCGTAGTGTCTCGTGTGGGCTTGGTGGGCAACTCGCTGGTC	240	
Qy	241	ATGTTCTGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTTACATATTTAAC	300	

Db 241 ATGTTCTGTCATCCGATACACAAAGATGAAGACAGCAACCAACATTACATATTAAC 300  
Qy 301 CTGGCTTGGCAGATGCTTTAGTACTACAAACCATGCCCTTTTCAGAGTAGGCTACTCTG 360  
Db 301 CTGGCTTGGCAGATGCTTTAGTACTACAAACCATGCCCTTTTCAGAGTAGGCTACTCTG 360  
Qy 361 ATGAATTCCTGGCTTTTGGGAGTGTCTGCAAGATAGTAATTTCCATTTGATTACTAC 420  
Db 361 ATGAATTCCTGGCTTTTGGGAGTGTCTGCAAGATAGTAATTTCCATTTGATTACTAC 420  
Qy 421 AACATGTTTACACAGATCTTCACTTGACCATGATGAGGTGACCGCTACATTTGCGGTG 480  
Db 421 AACATGTTTACACAGATCTTCACTTGACCATGATGAGGTGACCGCTACATTTGCGGTG 480  
Qy 481 TGCACCCCGTGAAGCTTTGGACTTCCGACACCCCTTGAAGCAAGATCATCAATATC 540  
Db 481 TGCACCCCGTGAAGCTTTGGACTTCCGACACCCCTTGAAGCAAGATCATCAATATC 540  
Qy 541 TGCATCTGGCTGTGCTGTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGCACCAAA 600  
Db 541 TGCATCTGGCTGTGCTGTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGCACCAAA 600  
Qy 601 GTCAGGAAGACGTGATGTCATGATGTCCTTTCAGATTCCTCCAGATGATGATCTACTCC 660  
Db 601 GTCAGGAAGACGTGATGTCATGATGTCCTTTCAGATTCCTCCAGATGATGATCTACTCC 660  
Qy 661 TGGTGGACCTCTTCATGATGATGTCCTTTCATGATGTCCTTTCATGATGATGATGATG 720  
Db 661 TGGTGGACCTCTTCATGATGATGTCCTTTCATGATGATGTCCTTTCATGATGATGATG 720  
Qy 721 ATCATCATCTGCTGCTACACCTGATGATCTCGTCTCAAGAGCTCGCGCTCTCTTTCT 780  
Db 721 ATCATCATCTGCTGCTACACCTGATGATCTCGTCTCAAGAGCTCGCGCTCTCTTTCT 780  
Qy 781 GGCTCCGAGAAAGATCCAACTCGGTGATGATCAGATGATGATGATGATGATGATGATG 840  
Db 781 GGCTCCGAGAAAGATCCAACTCGGTGATGATCAGATGATGATGATGATGATGATGATG 840  
Qy 841 GCAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
Db 841 GCAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
Qy 901 AGCAGCTCCACAGCAGCTGCTCTCTCCAGCTATTTACTTCTGCTGCTGCTGCTGCTGCT 960  
Db 901 AGCAGCTCCACAGCAGCTGCTCTCTCCAGCTATTTACTTCTGCTGCTGCTGCTGCTGCT 960  
Qy 961 ACCAAGTAGCTGATCCATCTCTAGCCTTTCTGATGAAATTTCAAGCGGTGT 1020  
Db 961 ACCAAGTAGCTGATCCATCTCTAGCCTTTCTGATGAAATTTCAAGCGGTGT 1020  
Qy 1021 TTCGGGACTTCTGCTTTCACATGAGATGAGGATGAGGCGGAGAGCTAGCAGATC 1080  
Db 1021 TTCGGGACTTCTGCTTTCACATGAGATGAGGATGAGGCGGAGAGCTAGCAGATC 1080  
Qy 1081 CGAAATACAGTTCCAGATCTGCTTACCTGAGGACATCGATGGGATGAATAACCAAGTA 1140  
Db 1081 CGAAATACAGTTCCAGATCTGCTTACCTGAGGACATCGATGGGATGAATAACCAAGTA 1140  
Qy 1141 TGACTAGTCTGTGA 1154  
Db 1141 TGACTAGTCTGTGA 1154

RESULT 7  
ADN30511 standard; cDNA; 1154 BP.  
XX ID  
XX AC  
XX ADN30511;  
DT 12-AUG-2004 (first entry)  
XX DE  
XX Human kappa opioid receptor, hKOR, C856T allele.  
XX

KW Human; kappa opioid receptor; hKOR; ss; gene; SNP;  
KW single nucleotide polymorphism; endogenous opioid system; nociception;  
KW neurotransmitter release; learning; memory; cognition; pain; cocaine;  
KW amphetamine; alcohol; tobacco; opiate; withdrawal;  
KW neuroendocrine function; reproductive function; prolactin regulation;  
KW stress responsiveness; mood; affect; immune function;  
KW gastrointestinal function; analgesia; additive disease;  
KW chromosome 8q11.2.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT allele replace(846,C)  
FT /\*tag= a  
FT /standard\_name= "Single nucleotide polymorphism"  
XX US2004097704-A1.  
XX  
PD 20-MAY-2004.  
XX  
PF 13-JUL-2001; 2001US-00904584.  
XX  
PR 14-JUL-2000; 2000US-0218300P.  
XX  
PA (KREE/) KREEK M J.  
XX (YUFE/) YUFEROV V.  
PA (LAFO/) LAFORGE K S.  
XX  
PI Kreek MJ, Yufarov V, Laforge KS;  
XX WPI; 2004-389204/36.  
DR  
XX  
PT Novel isolated variant allele of human kappa opioid receptor gene, useful  
PT for determining susceptibility in subject to physiological response,  
PT condition or disease related to endogenous opioid system.  
XX  
PS Example; SEQ ID NO 7; 29pp; English.  
XX

CC The invention relates to an isolated variant allele of a human kappa  
CC opioid receptor gene, comprising a DNA sequence having at least one  
CC variation in a fully defined wild-type allele of human kappa opioid  
CC receptor (hKOR) sequence appearing as ADN30505, where the variation  
CC comprises C852T, C948T or their combinations. Also included are  
CC an isolated nucleic acid molecule selectively hybridizing to the variant,  
CC a cloning vector comprising the variant and an origin of replication, an  
CC expression vector comprising the variant associated with a promoter, a  
CC unicellular host transformed/transfected with the vector and a commercial  
CC test kit for determining the presence of at least one variation in a hKOR  
CC gene of an allele in a bodily sample taken from a subject. The hKOR  
CC variant allele is useful for determining a susceptibility in a subject to  
CC at least one physiological response, condition or disease related to the  
CC endogenous opioid system, nociception, neurotransmitter release  
CC endogenous opioid system, learning, memory, cognition, pain, cocaine,  
CC amphetamine and other stimulants self-administration, behavioural  
CC sensitization to cocaine, opiates, alcohol and tobacco, opiate,  
CC amphetamine and alcohol withdrawal, physical dependence and tolerance;  
CC neuroendocrine function, reproductive function, prolactin regulation,  
CC stress responsiveness, physiology and pathology of mood and affect, immune  
CC function, gastrointestinal function. The hKOR variant allele is useful  
CC for determining a susceptibility to pain in a subject and is useful for  
CC determining a therapeutically effective amount of pain reliever to  
CC administer to a subject in order to induce analgesia in the subject. The  
CC hKOR variant allele is useful for determining a therapeutically effective  
CC amount of therapeutic agent to administer to a subject suffering from at  
CC least one addictive disease to treat the at least one addictive disease.  
CC The gene for hKOR is located on chromosome 8q11.2. The present sequence  
CC is the C846T allele of hKOR.  
XX  
SQ Sequence 1154 BP; 239 A; 338 C; 287 G; 290 T; 0 U; 0 Other;

Query Match 99.7%; Score 1150.8; DB 12; Length 1154;  
Best Local Similarity 99.8%; Pred. No. 5.9e-274; Indels 0; Gaps 0;  
Matches 1152; Conservative 0; Mismatches 2;

Qy	1	ATGGAATCCCGAGTCCAGACTCTTCGGCGGGAGCCGGGCCTTA	CCTTGCGGCCCGCAGCGCC	60
Db				
Qy	1	ATGGAATCCCGAGTCCAGACTCTTCGGCGGGAGCCGGGCCTTA	CCTTGCGGCCCGCAGCGCC	60
Db				
Qy	61	TGCCTTGCCCCCAACAGCAGCGCCCTGTGTTTCCC	GCGTGGCGCGAGCCCCGACAGCAAGCGC	120
Db				
Qy	61	TGCCTTGCCCCCAACAGCAGCGCCCTGTGTTTCCC	GCGTGGCGCGAGCCCCGACAGCAAGCGC	120
Db				
Qy	121	AGCGCCGCTCGAGGAGCGCGAGCTTGAGCGCCGGGACA	TCTCTCCCGGCCCATCCCGGTC	180
Db				
Qy	121	AGCGCCGCTCGAGGAGCGCGAGCTTGAGCGCCGGGACA	TCTCTCCCGGCCCATCCCGGTC	180
Db				
Qy	181	ATCATCACGGCGCTCTACTTCGCTAGTGTTCGTGCTGG	CTTGGTGGGCAACTCCGCTGGTC	240
Db				
Qy	181	ATCATCACGGCGCTCTACTTCGCTAGTGTTCGTGCTGG	CTTGGTGGGCAACTCCGCTGGTC	240
Db				
Qy	241	ATGTTTCGTGATCATCCGATACACAAAGATGAAGACAG	CAACCAACATTATATATTTAAC	300
Db				
Qy	241	ATGTTTCGTGATCATCCGATACACAAAGATGAAGACAG	CAACCAACATTATATATTTAAC	300
Db				
Qy	301	CTGGCTTTGGCAGATGCTTTTAGTTACTATCAACCAAT	AGCCCTTTCAGAGTACGGTCTACTTG	360
Db				
Qy	301	CTGGCTTTGGCAGATGCTTTTAGTTACTATCAACCAAT	AGCCCTTTCAGAGTACGGTCTACTTG	360
Db				
Qy	361	ATGAATTCCTCGCCCTTTTGGGGATGCTGTGCAAGAT	PAGTAATTTCCATTGATTACTAC	420
Db				
Qy	361	ATGAATTCCTCGCCCTTTTGGGGATGCTGTGCAAGAT	PAGTAATTTCCATTGATTACTAC	420
Db				
Qy	421	AACATGTTTACCAGCATCTTCACCTTGACCATGATGAG	CGGTGGACCGCTACATTCGCGTG	480
Db				
Qy	421	AACATGTTTACCAGCATCTTCACCTTGACCATGATGAG	CGGTGGACCGCTACATTCGCGTG	480
Db				
Qy	481	TGCCACCCCGTGAAGGCTTTTGGACTTTCCGCAAC	CCCTTGAAGGCAAGAATCATCAATATC	540
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Qy	481	TGCCACCCCGTGAAGGCTTTTGGACTTTCCGCAAC	CCCTTGAAGGCAAGAATCATCAATATC	540
Db				
Qy	541	TGCATCTGGCTGCTGTCTCATCTGTTGGCATCTCTG	CAATAGTCCTTGGAGGACCAAAA	600
Db				
Qy	541	TGCATCTGGCTGCTGTCTCATCTGTTGGCATCTCTG	CAATAGTCCTTGGAGGACCAAAA	600
Db				
Qy	601	GTCAGGGAAGACGTGATGTCAITTAGTGTCTCTTGC	AGTTTCCAGATGATGACTACTCC	660
Db				
Qy	601	GTCAGGGAAGACGTGATGTCAITTAGTGTCTCTTGC	AGTTTCCAGATGATGACTACTCC	660
Db				
Qy	661	TGTTGGGACCTTTCATGAAGATCTGGCTCTTCAAT	CTTTTGGCTTCGTGATCCCTGTGCTC	720
Db				
Qy	661	TGTTGGGACCTTTCATGAAGATCTGGCTCTTCAAT	CTTTTGGCTTCGTGATCCCTGTGCTC	720
Db				
Qy	721	ATCATCATGCTCTGCTACACCTCATGATCTCTGGT	CTCTCAAGAGCTTCGGCTCTCTTTCT	780
Db				
Qy	721	ATCATCATGCTCTGCTACACCTCATGATCTCTGGT	CTCTCAAGAGCTTCGGCTCTCTTTCT	780
Db				
Qy	781	GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGAT	CACAGACTTGGTCTGGTGGTGCTG	840
Db				
Qy	781	GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGAT	CACAGACTTGGTCTGGTGGTGCTG	840
Db				
Qy	841	GCAGTCTTCGTGCTGCTGAGCTCCCATTCACATA	TATTCATCTCTGGTGGAGGCTCTGGG	900
Db				
Qy	841	GCAGTCTTCGTGCTGCTGAGCTCCCATTCACATA	TATTCATCTCTGGTGGAGGCTCTGGG	900
Db				
Qy	901	AGCACCTCCACAGCAGCAGCTGCTCTCTCCAGCT	TATTACTCTGCATCGCCTTAGGCTAT	960
Db				
Qy	901	AGCACCTCCACAGCAGCAGCTGCTCTCTCCAGCT	TATTACTCTGCATCGCCTTAGGCTAT	960
Db				
Qy	961	ACCAACAGTAGCCTGAATCCCATTTCTCTACG	CCCTTTCTTGATGAAAAATTTCAAGCGGTGT	1020
Db				
Qy	961	ACCAACAGTAGCCTGAATCCCATTTCTCTACG	CCCTTTCTTGATGAAAAATTTCAAGCGGTGT	1020
Db				
Qy	1021	TTCCGGGACTTCTGCTTTTCCA	CTGAAGATGAGGATGGAGCGGACAGCACTAGCAGAGTC	1080
Db				
Qy	1021	TTCCGGGACTTCTGCTTTTCCA	CTGAAGATGAGGATGGAGCGGACAGCACTAGCAGAGTC	1080
Db				

Qy	1081	CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCACTGA	1140
Db	1081	CGAAATACAGTTCAGGATCCTGCTTACCTGAGGGACATCGATGGGATGAATAAACCACTGA	1140
Qy	1141	TGACTAGTCTGTGA	1154
Db	1141	TGACTAGTCTGTGA	1154
RESULT 8			
ADN30509			
ID	ADN30509 standard; cDNA; 1154 BP.		
XX			
AC	ADN30509;		
XX			
XX	12-AUG-2004 (first entry)		
XX			
DE	Human kappa opioid receptor, hKOR, G36T allele.		
XX			
KW	Human; kappa opioid receptor; hKOR; ss; gene; SNP;		
KW	single nucleotide polymorphism; endogenous opioid system; nociception;		
KW	neurotransmitter release; learning; memory; cognition; pain; cocaine;		
KW	amphetamine; alcohol; tobacco; opiate; withdrawal;		
KW	neuroendocrine function; reproductive function; prolactin regulation;		
KW	stress responsivity; mood; affect; immune function;		
KW	-gastrointestinal function; analgesia; addictive disease;		
KW	chromosome 8q11.2.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	allele	replace(36,G)	
FT		/*tag= a	
FT		/standard_name= "Single nucleotide polymorphism"	
XX			
PN	US2004097704-A1.		
XX			
PD	20-MAY-2004.		
XX			
PF	13-JUL-2001; 2001US-00904584.		
XX			
PR	14-JUL-2000; 2000US-0218300P.		
XX			
PA	(KREE/) KREEK M J.		
PA	(YUFE/) YUFEROV V.		
XX	(LAFO/) LAFORGE K S.		
XX			
PI	Kreek MJ, Yufarov V, Laforge KS;		
XX			
XX	WPI; 2004-389204/36.		
XX			
PT	Novel isolated variant allele of human kappa opioid receptor gene, useful		
PT	for determining susceptibility in subject to physiological response,		
PT	condition or disease related to endogenous opioid system.		
XX			
XX	Example; SEQ ID NO 5; 29pp; English.		
XX			
CC	The invention relates to an isolated variant allele of a human kappa		
CC	opioid receptor gene, comprising a DNA sequence having at least one		
CC	variation in a fully defined wild-type allele of human kappa opioid		
CC	receptor (hKOR) sequence appearing as ADN30505, where the variation		
CC	comprises C852T, C948T, C1008T or their combinations. Also included are		
CC	an isolated nucleic acid molecule selectively hybridising to the variant,		
CC	a cloning vector comprising the variant and an origin of replication, an		
CC	expression vector comprising the variant associated with a promoter, a		
CC	eucellular host transformed/transfected with the vector and a commercial		
CC	test kit for determining the presence of at least one variation in a hKOR		
CC	gene of an allele in a bodily sample taken from a subject. The hKOR		
CC	variant allele is useful for determining a susceptibility in a subject to		
CC	at least one physiological response, condition or disease related to the		
CC	endogenous opioid system, nociception, neurotransmitter release		
CC	endogenous opioid system, learning, memory, cognition, pain, cocaine,		
CC	amphetamine and other stimulants self-administration, behavioural		

CC sensitisation to cocaine, opiates, alcohol and tobacco, opiate,  
CC amphetamine and alcohol withdrawal, physical dependence and tolerance;  
CC neuroendocrine function, reproductive function, prolactin regulation,  
CC stress responsivity, physiology and pathology of mood and affect, immune  
CC function, gastrointestinal function. The hKOR variant allele is useful  
CC for determining a susceptibility to pain in a subject and is useful for  
CC determining a therapeutically effective amount of pain reliever to  
CC administer to a subject in order to induce analgesia in the subject. The  
CC hKOR variant allele is useful for determining a therapeutically effective  
CC amount of therapeutic agent to administer to a subject suffering from at  
CC least one addictive disease to treat the at least one addictive disease.  
CC The gene for hKOR is located on chromosome 8q11.2. The present sequence  
CC is the G36T allele of hKOR.  
XX  
SQ Sequence 1154 BP; 239 A; 339 C; 286 G; 290 T; 0 U; 0 Other;  
Query Match 99.7%; Score 1150.8; DB 12; Length 1154;  
Best Local Similarity 99.8%; Pred. No. 5.9e-274;  
Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 ATGGACTCCCGATCCAGATCTTCGCGGGGAGCCGGCCCTACTCGCGCCCGAGCGCC 60  
DB 1 ATGGACTCCCGATCCAGATCTTCGCGGGGAGCCGGCCCTACTCGCGCCCGAGCGCC 60  
QY 61 TGCTGCCCCCAACAGCAGCGCTGCTTTCCCGGCTGGGCCGAGCCCGACAGCAACGCG 120  
DB 61 TGCTGCCCCCAACAGCAGCGCTGCTTTCCCGGCTGGGCCGAGCCCGACAGCAACGCG 120  
QY 121 AGCGCCGGCTCGGAGGACGCGAGCTGGAGCCCGCGCACATCTCCCGGCCCATCCCGGTC 180  
DB 121 AGCGCCGGCTCGGAGGACGCGAGCTGGAGCCCGCGCACATCTCCCGGCCCATCCCGGTC 180  
QY 181 ATCATCAGCGGCTCTACTCCGTAGTTCGCTGGGGCTGGCGCAACTCGCTGGTC 240  
DB 181 ATCATCAGCGGCTCTACTCCGTAGTTCGCTGGGGCTGGCGCAACTCGCTGGTC 240  
QY 241 ATGTTCTGTGATATCCGATACACAAAGATGAACAGCAACCAATTTACATATTTAAC 300  
DB 241 ATGTTCTGTGATATCCGATACACAAAGATGAACAGCAACCAATTTACATATTTAAC 300  
QY 301 CTGGCTTTGGCAGATGCTTTAGTATCTAACCAATGCCCTTTTCCAGAGTACGCTACTTG 360  
DB 301 CTGGCTTTGGCAGATGCTTTAGTATCTAACCAATGCCCTTTTCCAGAGTACGCTACTTG 360  
QY 361 ATGAATTCCTGGCTTTGGGATGCTGTCGACAGATGTAATTTCCATGATTAATCTAC 420  
DB 361 ATGAATTCCTGGCTTTGGGATGCTGTCGACAGATGTAATTTCCATGATTAATCTAC 420  
QY 421 AACATGTTTCCACAGCATCTTTCACCTTGACCATGATGAGCGTGACCGCTACATTCGCGTG 480  
DB 421 AACATGTTTCCACAGCATCTTTCACCTTGACCATGATGAGCGTGACCGCTACATTCGCGTG 480  
QY 481 TGGCACCCTGTAAGGCTTTGGACTTCGCGCACACCTTTGAAGGAAAGATCATCAATATC 540  
DB 481 TGGCACCCTGTAAGGCTTTGGACTTCGCGCACACCTTTGAAGGAAAGATCATCAATATC 540  
QY 541 TGATCTGGCTGCTGCTGCTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGACCAAA 600  
DB 541 TGATCTGGCTGCTGCTGCTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGACCAAA 600  
QY 601 GTGAGGGAAGACGTCGATGTCATGTCAGTGTCTTGCAGTTCCTGAGTATGATCACTCC 660  
DB 601 GTGAGGGAAGACGTCGATGTCATGTCAGTGTCTTGCAGTTCCTGAGTATGATCACTCC 660  
QY 661 TGGTGGGACCTTTCATGAAGATCTGCTCTTCACTTTTGGCTTCGTCGTCCTTCCTC 720  
DB 661 TGGTGGGACCTTTCATGAAGATCTGCTCTTCACTTTTGGCTTCGTCGTCCTTCCTC 720  
QY 721 ATCATATCTGCTCTACACCTCATGATCTGCTGGTCTCAAGAGCGTCCGGCTCTTCT 780  
DB 721 ATCATATCTGCTCTACACCTCATGATCTGCTGGTCTCAAGAGCGTCCGGCTCTTCT 780  
QY 781 GGCTCCCGAGAGAAAGATCGCAACCTCGGTAGGATCACAGACTGGTCTCTGGTGGTG 840

DB 781 GGCTCCCGAGAGAAAGATCGCAACCTCGGTAGGATCACAGACTGGTCTCTGGTGGTG 840  
QY 841 GGAGTCTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 900  
DB 841 GGAGTCTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 900  
QY 901 AGCACCCTCCACAGCAGCAGCTGCTCTCCAGCTATTAATCTTCTGTCATCGCCTTAGGCTAT 960  
DB 901 AGCACCCTCCACAGCAGCAGCTGCTCTCCAGCTATTAATCTTCTGTCATCGCCTTAGGCTAT 960  
QY 961 ACCAAACAGTAGCTTCCCAATCTTCTACGCTTTCTTGATGAAAATTTCAAGCGGTGT 1020  
DB 961 ACCAAACAGTAGCTTCCCAATCTTCTACGCTTTCTTGATGAAAATTTCAAGCGGTGT 1020  
QY 1021 TTCCGGGACTTCTGCTTCCCAATGAGATGAGGATGAGGATGAGGATGAGGATGAGGATG 1080  
DB 1021 TTCCGGGACTTCTGCTTCCCAATGAGATGAGGATGAGGATGAGGATGAGGATGAGGATG 1080  
QY 1081 CGAAATACAGTTCAGGATCTGCTTACCTGAGGACATCGATGGGATGAATAAACAGTA 1140  
DB 1081 CGAAATACAGTTCAGGATCTGCTTACCTGAGGACATCGATGGGATGAATAAACAGTA 1140  
QY 1141 TGACTAGTGGTGA 1154  
DB 1141 TGACTAGTGGTGA 1154  
RESULT 9  
AB242678  
ID AB242678 standard; DNA; 1182 BP.  
XX  
AC AB242678;  
XX  
DT 04-MAR-2003 (first entry)  
XX  
DE Human opioid receptor kappa 1 nucleotide SEQ ID NO:147.  
XX  
KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
KW G protein-coupled receptor modulator; antibody; immune-related disease;  
KW growth-related disease; cell regeneration-related disease; autoimmune disease;  
KW immunological-related cell proliferative disease; osteoarthritis; allergy;  
KW Alzheimer's disease; atherosclerosis; infection; Crohn's disease; diabetes;  
KW osteoporosis; cardiomyopathy; inflammation; Parkinson's disease; multiple sclerosis; pain;  
KW graft versus host disease; depression; schizophrenia; dementia; memory loss;  
KW psoriasis; anxiety; depression; Parkinson's disease; multiple sclerosis; pain;  
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
KW ulcer; gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200261087-A2.  
XX  
PD 08-AUG-2002.  
XX  
PF 19-DEC-2001; 2001WO-US050107.  
XX  
PR 19-DEC-2000; 2000US-0257144P.  
XX  
PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
XX  
PI Burmer GC, Roush CL, Brown JP;  
XX  
DR WPI: 2003-046718/04.  
DR P-PSDB; ABP81832.  
XX  
PT New isolated antigenic peptides e.g., for G protein-coupled receptors  
PT (GPCR), useful for diagnosing and designing drugs for treating conditions  
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or  
PT autoimmune diseases.  
XX  
PS Disclosure; Fig 1; 523pp; English.

XX The present invention describes antigenic peptides (I) comprising: (a)  
 CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
 CC acids. Also described: (1) an assay for the detection of a particular G  
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
 CC and (2) an isolated antibody having high specificity and high affinity or  
 CC avidity for a particular GPCR. (1) can be used as GPCR modulators and in  
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an  
 CC antibody against a particular GPCR, and in the production of specific  
 CC antibodies. The peptides and antibodies are also useful for detecting the  
 CC presence or absence of corresponding GPCRs. The antigenic peptides for  
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for  
 CC treating immune-related diseases, growth-related diseases, cell  
 CC regeneration-related disease, immunological-related cell proliferative  
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,  
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host  
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory  
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,  
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
 CC any other disorder in which GPCRs are involved. The antibodies may be  
 CC used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode  
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 1182 BP; 245 A; 345 C; 293 G; 299 T; 0 U; 0 Other;

Query Match 99.2%; Score 1144.4; DB 8; Length 1182;  
 Best Local Similarity 99.5%; Pred. No. 2.3e-272;  
 Matches 1148; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGGACTCCCGATCCAGATCTTCGCGGGGAGCGCGCCCTACCTCGCGCCCGAGCGCC 60  
 DB 14 ATGGAATCCCGATTCAGATCTTCGCGGGGAGCGCGCCCTACCTCGCGCCCGAGCGCC 73  
 QY 61 TGCCTGCCCGCCCAACAGCAGCGCCCTGGTTTCCCGGCTGGCGGAGCGCGAGCAACCGC 120  
 DB 74 TGCCTGCCCGCCCAACAGCAGCGCCCTGGTTTCCCGGCTGGCGGAGCGCGAGCAACCGC 133  
 QY 121 AGCGCGCGCTGGAGGAGCGCGAGCTGGAGCGCGCGGCGACATCTCCCGGCGCATCCCGGTC 180  
 DB 134 AGCGCGCGCTGGAGGAGCGCGAGCTGGAGCGCGCGGCGACATCTCCCGGCGCATCCCGGTC 193  
 QY 181 ATCATCAGCGCGGTCTACTCCGTACTGTTCGTCGGGCTGGTGGGCAACTCCGCTGTC 240  
 DB 194 ATCATCAGCGCGGTCTACTCCGTACTGTTCGTCGGGCTGGTGGGCAACTCCGCTGTC 253  
 QY 241 ATGTTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAATTTACATATTTAAC 300  
 DB 254 ATGTTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAATTTACATATTTAAC 313  
 QY 301 CTGGCTTTGGCAGATGCTTTAGTTACTACAAACATGACCGCTTCAGAGTACGGTCTACTTG 360  
 DB 314 CTGGCTTTGGCAGATGCTTTAGTTACTACAAACATGACCGCTTCAGAGTACGGTCTACTTG 373  
 QY 361 ATGAATTCCTGGCCCTTTGGGAGTGTCTGTGCAAGATAGTAATTTCCATTTGATTACTAC 420  
 DB 374 ATGAATTCCTGGCCCTTTGGGAGTGTCTGTGCAAGATAGTAATTTCCATTTGATTACTAC 433  
 QY 421 AACATGTTTCCAGCAGCATCTTACCTTTGACCATGATGAGCGGTGGACCGGTACATTTGCCGTG 480  
 DB 434 AACATGTTTCCAGCAGCATCTTACCTTTGACCATGATGAGCGGTGGACCGGTACATTTGCCGTG 493  
 QY 481 TGCCACCCCGTGAAGGCTTTGGAGCTTCGCGACACCCCTTTGAAGGCAAGATCATCAATATC 540  
 DB 494 TGCCACCCCGTGAAGGCTTTGGAGCTTCGCGACACCCCTTTGAAGGCAAGATCATCAATATC 553  
 QY 541 TGCATCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
 DB 554 TGCATCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 613

QY 601 GTACGGGAGAGCGTCGATGTGTCATTCAGTGTCTCTTCGAGTGTCTCCAGAGTATCCAGAGTACTACTCC 660  
 DB 614 GTACGGGAGAGCGTCGATGTGTCATTCAGTGTCTCTTCGAGTGTCTCCAGAGTATCCAGAGTACTACTCC 673  
 QY 661 TGGTGGGACCTTTCATGAGATCGCGTCTTCATCTTTGCTTGGCTTGGTATCCCTGCTCTC 720  
 DB 674 TGGTGGGACCTTTCATGAGATCGCGTCTTCATCTTTGCTTGGCTTGGTATCCCTGCTCTC 733  
 QY 721 ATCATCATCTGCTGTCTACACCTCATGATCTCGGTCTCTCAAGAGCGTCCGGCTCTCTTCT 780  
 DB 734 ATCATCATCTGCTGTCTACACCTCATGATCTCGGTCTCTCAAGAGCGTCCGGCTCTCTTCT 793  
 QY 781 GGCTCCCGAGAGAAAGATCGCAACCTCGTAGGATCACAGACTGGTCTCTGGTGGTGTG 840  
 DB 794 GGCTCCCGAGAGAAAGATCGCAACCTCGTAGGATCACAGACTGGTCTCTGGTGGTGTG 853  
 QY 841 GCAGTCTTCGCTGCTGTGCTGACTCCCATTCACATATTCATCTTCATCTTCGCTGGAGGCTCTGGGG 900  
 DB 854 CGGTTTTTCGCTGCTGTGCTGACTCCCATTCACATATTCATCTTCGCTGGAGGCTCTGGGG 913  
 QY 901 AGCACTCCCAACAGCAGACTGCTCTCTCCAGCTATTACTTCTGCATCGCTTAGGCTAT 960  
 DB 914 AGCACTCCCAACAGCAGACTGCTCTCTCCAGCTATTACTTCTGCATCGCTTAGGCTAT 973  
 QY 961 ACCAACAGTAGCTGAATCCCATCTCTACCGCTTTCTTGATGAAATTTCAAGCGGTGT 1020  
 DB 974 ACCAACAGTAGCTGAATCCCATCTCTACCGCTTTCTTGATGAAATTTCAAGCGGTGT 1033  
 QY 1021 TTCCGGGACTTCTGCTTTCAGCTGAGATGAGATGAGGCGGAGAGCACTAGCAGAGTC 1080  
 DB 1034 TTCCGGGACTTCTGCTTTCAGCTGAGATGAGGCGGAGAGCACTAGCAGAGTC 1093  
 QY 1081 CGAAATACAGTTACAGGATCTGCTTACTGAGGAGACATCGATGGGATGAATAAACCACTA 1140  
 DB 1094 CGAAATACAGTTACAGGATCTGCTTACTGAGGAGACATCGATGGGATGAATAAACCACTA 1153  
 QY 1141 TGACTAGTCTGTGA 1154  
 DB 1154 TGACTAGTCTGTGA 1167  
 RESULT 10  
 AAD58490  
 ID AAD58490 standard; DNA; 1182 BP.  
 XX  
 AC AAD58490;  
 XX  
 DT 04-DEC-2003 (first entry)  
 XX  
 DE Human kappa opioid receptor 1 (KOR) DNA.  
 XX  
 KW Human; neurological disorder; urinary incontinence; gene therapy; cancer;  
 KW kidney disorder; overactive; oversensitive bladder; dysfunction; bladder;  
 KW urethra; overflow urinary incontinence; stress urinary incontinence;  
 KW nervous system; prostatitis; benign prostatic hyperplasia; nephrotrophic;  
 KW kappa opioid receptor 1; KOR; gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 CDS 14..1156  
 FT /\*tag= a  
 FT /product= "Human kappa opioid receptor 1 (KOR)"  
 FT /note= "The CDS is referred to as SEQ ID NO:21 in the  
 specification"  
 FT  
 FT WO2003061573-A2.  
 FN  
 FN 31-JUL-2003.  
 PD  
 XX 16-JAN-2003; 2003WO-US001450.  
 PF  
 XX 18-JAN-2002; 2002US-0349511P.  
 PR

28-FEB-2002; 2002US-0360500P.  
 15-MAR-2002; 2002US-0365041P.  
 19-APR-2002; 2002US-0374063P.  
 14-AUG-2002; 2002US-0403468P.  
 27-SEP-2002; 2002US-0414262P.  
 21-OCT-2002; 2002US-0419986P.  
 05-NOV-2002; 2002US-0423809P.  
 26-NOV-2002; 2002US-0429797P.  
 (MILL-) MILLENNIUM PHARM INC.  
 Silos-Santiago I, Karicheti V;  
 WPI; 2003-598705/56.  
 P-PSDB; AAE38589.  
 Identifying a compound for treating urological disorders, for example  
 PT urinary incontinence by assaying the ability of the compound to modulate  
 PT the nucleic acid expression or polypeptide activity.  
 XX  
 PS Disclosure; Page 149-151; Opp; English.  
 XX  
 CC The present relates to a method for identifying a compound for treating  
 CC urological disorders e.g., urinary incontinence including overactive/  
 CC over-sensitive bladder, overflow urinary incontinence, stress urinary  
 CC incontinence caused by dysfunction of the bladder, urethra or central  
 CC peripheral nervous system, prostatitis, benign prostatic hyperplasia,  
 CC cancer of the prostate or kidney disorders. The method is also useful for  
 CC modulating hyperplasia in a cell and treating a subject having a  
 CC urological disorder. The invention is also used in gene therapy. The  
 CC present sequence is human kappa opioid receptor 1 (KOR) DNA  
 XX  
 SQ Sequence 1182 BP; 245 A; 345 C; 293 G; 299 T; 0 U; 0 Other;  
 Query Match 99.2%; Score 1144.4; DB 10; Length 1182;  
 Best Local Similarity 99.5%; Pred. No. 2.3e-272;  
 Matches 1148; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 1 ATGGACTCCCGATCAGATCTTCCGGGGAGCGCGGCTTACCTGCGCGCCGAGCGGC 60  
 14 ATGGAATCCCGATTCAGATCTTCCGGGGAGCGCTGGCCCTACCTGCGCGCCGAGCGGC 73  
 61 TGCTGCGCGCCCAACAGCAGCGCTGGTTTCCGGGCTGGCGCCGAGCGCCAGCAACGCGC 120  
 74 TGCTGCGCGCCCAACAGCAGCGCTGGTTTCCGGGCTGGCGCCGAGCGCCAGCAACGCGC 133  
 121 AGCGCGCGCTCGGAGGACGCGAGCTGGAGCGCGGACATCTCCCGCGCATCCCGGTC 180  
 134 AGCGCGCGCTCGGAGGACGCGAGCTGGAGCGCGGACATCTCCCGCGCATCCCGGTC 193  
 181 ATCATCAGCGCGCTTACTCCGTAGTGTTCGTGTTGGGCTTGGTGGGCACTCGCTGGTC 240  
 194 ATCATCAGCGCGCTTACTCCGTAGTGTTCGTGTTGGGCTTGGTGGGCACTCGCTGGTC 253  
 241 ATGTTCTGTATCATCCGATACACAGATGAGACGACCAACCAATTTACATATTAAAC 300  
 254 ATGTTCTGTATCATCCGATACACAGATGAGACGACCAACCAATTTACATATTAAAC 313  
 301 CTGGCTTTGGCAGATGCTTTAGTTACTACCAACATGCGCCCTTTAGAGTACGGTCTACTTG 360  
 314 CTGGCTTTGGCAGATGCTTTAGTTACTACCAACATGCGCCCTTTAGAGTACGGTCTACTTG 373  
 361 ATGAATCTCGGCTTTGGGATGTCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420  
 374 ATGAATCTCGGCTTTGGGATGTCTGTGCAAGATAGTAATTTCCATTGATTACTAC 433  
 421 AACATGTTCCACGATCTTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCGGTG 480  
 434 AACATGTTCCACGATCTTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCGGTG 493  
 481 TGGCACCCCGTGAGGCTTTGGATTCGCGACACCCCTTGAAGGCAAGATCATCATATC 540  
 494 TGGCACCCCGTGAGGCTTTGGATTCGCGACACCCCTTGAAGGCAAGATCATCATATC 553

QY 541 TGCATCTGGCTGCTGCTCATCTCTTGGCATCTCTGCAATAGTCTCTTGGAGGACCCAAA 600  
 DB 554 TGCATCTGGCTGCTGCTGCTCATCTCTTGGCATCTCTGCAATAGTCTCTTGGAGGACCCAAA 613  
 QY 601 GTGAGGGAAGAGCTCGATGTCATTTGAGTGCTCTTTGCGAGTTCCAGATGATGACTACTCC 660  
 DB 614 GTGAGGGAAGAGCTCGATGTCATTTGAGTGCTCTTTGCGAGTTCCAGATGATGACTACTCC 673  
 QY 661 TGGTGGGACCTCTTTCATGAAGATCTGGGTCTTTCATCTTTTGCCTTGGTATCCTGCTCTC 720  
 DB 674 TGGTGGGACCTCTTTCATGAAGATCTGGGTCTTTCATCTTTTGCCTTGGTATCCTGCTCTC 733  
 QY 721 ATCATCATGCTGCTGTACACCTGATGATCTCGCTCTCAAGAGCGTCCGGCTCTCTTCT 780  
 DB 734 ATCATCATGCTGCTGTACACCTGATGATCTCGCTCTCAAGAGCGTCCGGCTCTCTTCT 793  
 QY 781 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACAGACTGGTCTGTTGGTGGTG 840  
 DB 794 GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACAGACTGGTCTGTTGGTGGTG 853  
 QY 841 GGAGTCTTGGTCTGCTGTGGACTCCCATTCATATTCATCTCTGATCGCTTAGGCTAT 900  
 DB 854 GCGGTTTTGCTGCTGTGGACTCCCATTCATATTCATCTCTGATCGCTTAGGCTAT 913  
 QY 901 AGCACTCCCGAGAGAGCTGCTCTCTCCAGCTATTACTTCTGATCGCTTAGGCTAT 960  
 DB 914 AGCACTCCCGAGAGAGCTGCTCTCTCCAGCTATTACTTCTGATCGCTTAGGCTAT 973  
 QY 961 ACCAAGAGTAGCTGAATCCCAATCTCTACGCTTTCTTGTGATAAATTTCAAGCGGTG 1020  
 DB 974 ACCAAGAGTAGCTGAATCCCAATCTCTACGCTTTCTTGTGATAAATTTCAAGCGGTG 1033  
 QY 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGAGTGGAGCGGAGCACTAGCAGAGTC 1080  
 DB 1034 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGAGTGGAGCGGAGCACTAGCAGAGTC 1093  
 QY 1081 CGAATATACAGTTTCAAGATCTGCTTACCTGAGGACATCGATGGATGAATAAACAGTA 1140  
 DB 1094 CGAATATACAGTTTCAAGATCTGCTTACCTGAGGACATCGATGGATGAATAAACAGTA 1153  
 QY 1141 TCACTAGTCTGGA 1154  
 DB 1154 TCACTAGTCTGGA 1167  
 RESULT 11  
 ADE84861  
 ID ADE84861 standard; DNA; 1182 BP.  
 XX  
 AC ADE84861;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Farnesyl transferase inhibitor modulated leukemia associated gene #80.  
 XX ss: cytostatic; farnesyl transferase inhibitor; gene expression;  
 XX quinolone; leukemia; cancer.  
 XX Homo sapiens.  
 XX OS  
 XX PN WO2003038129-A2.  
 XX PD 08-MAY-2003.  
 XX PF 30-OCT-2002; 2002WO-US034784.  
 XX PR 30-OCT-2001; 2001US-0338997P.  
 XX PR 30-OCT-2001; 2001US-0340081P.  
 XX PR 30-OCT-2001; 2001US-0340938P.  
 XX PR 30-OCT-2001; 2001US-0341012P.  
 XX  
 PA (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.



XX Raponi M;  
 XX WPI; 2003-513497/48.  
 XX Determining whether a patient will respond to treatment with a farnesyl  
 XX transferase inhibitor, by analyzing the expression of gene that is  
 XX differentially modulated in the presence of the inhibitor.  
 XX Disclosure; SEQ ID NO 80; 346pp; English.  
 XX The invention relates to a method of determining whether a patient will  
 XX respond to treatment with a farnesyl transferase inhibitor (FTI), by  
 XX analyzing the expression of gene that is differentially modulated in the  
 XX presence of an FTI. The method is useful for determining whether a  
 XX patient will respond to treatment with a FTI such as (B)-6-[amino(4-  
 XX chlorophenyl)(1-methyl-1H-imidazol-5-yl)methyl]-4-(3-chlorophenyl)-1-  
 XX methyl-2-(1H)quinolinone, monitoring the therapy of a patient, treating a  
 XX patient with leukemia with FTI if the analysis indicates that the patient  
 XX will respond. This sequence corresponds to a gene whose expression may be  
 XX modulated in the presence of FTI.  
 XX SQ Sequence 1182 BP; 245 A; 345 C; 293 G; 299 T; 0 U; 0 Other;  
 Query Match 99.2%; Score 1144.4; DB 10; Length 1182;  
 Best Local Similarity 99.5%; Pred. No. 2.3e-272;  
 Matches 1148; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 ATGGACTCCCGATCCAGATCTTCGCGGGGAGCGGCGCCCTACTCGGCGCCCGAGCGCC 60  
 DB 14 ATGAATCCCGATTTCAGATCTTCGCGGGGAGCGCTGGCCCTACTCGGCGCCCGAGCGCC 73  
 QY 61 TGCCTGCCCCCAACAGCAGCGCCCTGGTTTCCCGGCTGGCGCGAGCCCGCAGCAACGGC 120  
 DB 74 TGCCTGCCCCCAACAGCAGCGCCCTGGTTTCCCGGCTGGCGCGAGCCCGCAGCAACGGC 133  
 QY 121 AGCGCGGCTCGAGGAGCGCGAGCTGGAGCGCGCGCAGCATCTCCCGCGCCATCCCGGTC 180  
 DB 134 AGCGCGGCTCGAGGAGCGCGAGCTGGAGCGCGCGCAGCATCTCCCGCGCCATCCCGGTC 193  
 QY 181 ATCATCAGCGGCTACTCCGTAAGTGTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 240  
 DB 194 ATCATCAGCGGCTACTCCGTAAGTGTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 253  
 QY 241 ATGTTCTGTGATCATCCGATACACAAAGATGAAGCAGCAACCAATTCATATTTAAAC 300  
 DB 254 ATGTTCTGTGATCATCCGATACACAAAGATGAAGCAGCAACCAATTCATATTTAAAC 313  
 QY 301 CTGCTTTGGCAGATGCTTTTACTACTACAAACCATGCCCTTTTCAGAGTACGCTCTACTTG 360  
 DB 314 CTGCTTTGGCAGATGCTTTTACTACTACAAACCATGCCCTTTTCAGAGTACGCTCTACTTG 373  
 QY 361 ATGAATTCCTGGCCTTTGGGATGTCGTGCAAGATAGTAATTTCCATTGATTACTAC 420  
 DB 374 ATGAATTCCTGGCCTTTGGGATGTCGTGCAAGATAGTAATTTCCATTGATTACTAC 433  
 QY 421 AACATGTTCCAGCAGCATCTTCACTTGACCATGATGAGCGTGGACCGCTACATGCGGTG 480  
 DB 434 AACATGTTCCAGCAGCATCTTCACTTGACCATGATGAGCGTGGACCGCTACATGCGGTG 493  
 QY 481 TGCCACCCCGTGAAGGCTTTGGATCTCCGACACCCCTTTGAAGGCAAGATCATCAATATC 540  
 DB 494 TGCCACCCCGTGAAGGCTTTGGATCTCCGACACCCCTTTGAAGGCAAGATCATCAATATC 553  
 QY 541 TGATCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
 DB 554 TGATCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 613  
 QY 601 GTACAGGGAAGACGTCGATGTCATTCAGTGTCCCTTGGAGTTCAGATGATGATCTCTCC 660  
 DB 614 GTACAGGGAAGACGTCGATGTCATTCAGTGTCCCTTGGAGTTCAGATGATGATCTCTCC 673  
 QY 661 TGGTGGGACCTCTTTCATGAAGATCTGCGTCTTTCATCTTTGCGCTTCGTGATCCCTGCTC 720

DB 674 TGGTGGGACCTCTTTCATGAAGATCTGCGTCTTTCATCTTTGCGTTCGTGATCCCTGCTC 733  
 QY 721 ATCATCATCGTCTGCTACACCTCATGATCTGCGTCTCAAGAGGTCGCGCTCCTTTCT 780  
 DB 734 ATCATCATCGTCTGCTACACCTCATGATCTGCGTCTCAAGAGGTCGCGCTCCTTTCT 793  
 QY 781 GGCCTCCGAGAGAAAGATCGCAACCTGCTAGGATCACAGACTGGTCTCTGCTGGTGTG 840  
 DB 794 GGCCTCCGAGAGAAAGATCGCAACCTGCTAGGATCACAGACTGGTCTCTGCTGGTGTG 853  
 QY 841 GCAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
 DB 854 GCGGTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 913  
 QY 901 AGCACTCTCCACACAGCAGCTGCTCTCTCCAGCTATTACTTCTCATCGCTCTAGGCTAT 960  
 DB 914 AGCACTCTCCACACAGCAGCTGCTCTCTCCAGCTATTACTTCTCATCGCTCTAGGCTAT 973  
 QY 961 ACCAACAGTAGCTGAATCCCATTTCTTACGCCCTTTCTTATGAAATTTTCAAGCGGTG 1020  
 DB 974 ACCAACAGTAGCTGAATCCCATTTCTTACGCCCTTTCTTATGAAATTTTCAAGCGGTG 1033  
 QY 1021 TTCCGGGACTTCTGCTTTTCCATCTGAAGATGAGGATGAGCGGCGAGCAGCTAGCAGATC 1080  
 DB 1034 TTCCGGGACTTCTGCTTTTCCATCTGAAGATGAGGATGAGCGGCGAGCAGCTAGCAGATC 1093  
 QY 1081 CGAATACAGTTTCAAGATCTGCTTACCTGAGGAGATGAGCGGCGAGCAGCTAGCAGATC 1140  
 DB 1094 CGAATACAGTTTCAAGATCTGCTTACCTGAGGAGATGAGCGGCGAGCAGCTAGCAGATC 1153  
 QY 1141 TGACTAGTCTGTGA 1154  
 DB 1154 TGACTAGTCTGTGA 1167  
 RESULT 12  
 ACAS6819  
 ID ACAS6819 standard; cDNA; 1182 BP.  
 XX ACAS6819;  
 XX 06-JUN-2003 (first entry)  
 DT Human signalling pathway polynucleotide probe SEQ ID NO 1417.  
 DE Human; probe; ss; array element; Parkinson's disease;  
 KW signalling pathway population; cancer; adenocarcinoma; leukaemia;  
 KW immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.  
 XX Homo sapiens.  
 XX US6500938-B1.  
 XX 31-DEC-2002.  
 XX 30-JAN-1998; 98US-00016434.  
 XX 30-JAN-1998; 98US-00016434.  
 XX (INCY-) INCYTE GENOMICS INC.  
 XX Au-Young J, Seilhamer JJ;  
 XX WPI; 2003-352189/33.  
 XX Combination of polynucleotide probes, useful as array elements in a  
 XX microarray for monitoring the expression of a number of target  
 XX polynucleotides.  
 XX Claim 1; SEQ ID NO 1417; 65pp; English.  
 XX The invention relates to a combination which, comprises a number of



polynucleotide probes comprising a sequence selected from one of the 1490 sequences mentioned in the specification. The combination is useful as an array element in a microarray for monitoring the expression of a number of target polynucleotides. The microarray is particularly useful in the diagnosis and treatment of cancer and immunopathology and neuropathology. The microarray is useful in diagnostics and treatment regimens, drug discovery and development, toxicological and carcinogenicity studies, forensics and pharmacogenomics. The microarray is also useful for monitoring progression of diseases and for developing sophisticated profiles for the effects of currently available therapeutic drugs. The combination is also useful for purifying a subpopulation of mRNAs, cDNAs and genomic fragments and in research and diagnostic applications. The array can detect changes in expression in a large number of genes coding for different signaling pathway populations which can be used to diagnose various diseases including cancer e.g. adenocarcinoma and leukaemia, immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease and Parkinson's disease. The present sequence represents a polynucleotide probe of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at [seqdata.uspto.gov/sequence.html?DocID=06500938B1](http://seqdata.uspto.gov/sequence.html?DocID=06500938B1)

XX Sequence 1182 BP; 245 A; 345 C; 293 G; 299 T; 0 U; 0 Other;

Query Match 99.2%; Score 1144.4; DB 10; Length 1182;  
 Best Local Similarity 99.5%; Pred. No. 2.3e-272;  
 Matches 1148; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGGACTCCCGATCCAGATCTTCCCGGGGAGCGCGGCTTACCTTGCCTCCCGAGCGGC 60  
 DB 14 ATGGAATCCCGATTCCAGATCTTCCCGGGGAGCGCTTACCTTGCCTCCCGAGCGGC 73  
 QY 61 TGCTGCCCCCACAAGCGCGCTGTTCCCGGCTGGCGGAGCCGACGACGACGCGC 120  
 DB 74 TGCTGCCCCCACAAGCGCGCTGTTCCCGGCTGGCGGAGCCGACGACGACGCGC 133  
 QY 121 AGCGCGGCTCGGAGGACGCGAGCTGGAGCGCGCCGACATCTCCCGCGCCATCCCGGTC 180  
 DB 134 AGCGCGGCTCGGAGGACGCGAGCTGGAGCGCGCCGACATCTCCCGCGCCATCCCGGTC 193  
 QY 181 ATCATCAGCGCGTCTACTCCGAGTGTGCTGCTGGGCTTGGTGGGCACTCGCTGGTC 240  
 DB 194 ATCATCAGCGCGTCTACTCCGAGTGTGCTGCTGGGCTTGGTGGGCACTCGCTGGTC 253  
 QY 241 ATGTCGTGATCATCCGATACAAAGATGAGACAGACGACCAACATTTACATATTAC 300  
 DB 254 ATGTCGTGATCATCCGATACAAAGATGAGACAGACCAACATTTACATATTAC 313  
 QY 301 CTGGCTTTGGCAGATGCTTTAGTACTCAACCATGCGCTTTCAAGATGAGTCTACTTG 360  
 DB 314 CTGGCTTTGGCAGATGCTTTAGTACTCAACCATGCGCTTTCAAGATGAGTCTACTTG 373  
 QY 361 ATGAATTCCTGGCTTTGGGAGTGTGCTGCAAGATAGTAATTTCCATTTGATTAATAC 420  
 DB 374 ATGAATTCCTGGCTTTGGGAGTGTGCTGCAAGATAGTAATTTCCATTTGATTAATAC 433  
 QY 421 AACATGTTACAGCATCTTACATGACCATGAGCGTGACCGCTACATTTGCGGTG 480  
 DB 434 AACATGTTACAGCATCTTACATGACCATGAGCGTGACCGCTACATTTGCGGTG 493  
 QY 481 TGCACCCCGTGAAGCTTTGGAGTTCGCGACACCCCTTGAAGGCAAGATCATCAATATC 540  
 DB 494 TGCACCCCGTGAAGCTTTGGAGTTCGCGACACCCCTTGAAGGCAAGATCATCAATATC 553  
 QY 541 TGATCTGGTGTGCTGCTCATCTGTTGGCATCTTGCAATAGTCTTGGAGGACCAAA 600  
 DB 554 TGATCTGGTGTGCTGCTCATCTGTTGGCATCTTGCAATAGTCTTGGAGGACCAAA 613  
 QY 601 GTCAGGAGACCTCGATGCTATTGATGCTCTTCCAGTTCAGATGATGACTACTCC 660  
 DB 614 GTGAGGAGACCTCGATGCTATTGATGCTCTTCCAGTTCAGATGATGACTACTCC 673  
 QY 661 TGGTGGGACCTCTTCAATGAAGATCTGCGTCTTTCATCTTTTGCCTTTCGTGATCCCTGTCCTC 720

DB 674 TGGTGGGACCTTTTCATGAAGATCTGCGTCTTTCATCTTTCGCTTTCGCTGATCCCTGCTTC 733  
 QY 721 ATCATCATCGTCTGTACACCTGTGATCTCTGCGCTCTCAAGAGCGTCCGGCTCTTCT 780  
 DB 734 ATCATCATCGTCTGTACACCTGTGATCTCTGCGCTCTCAAGAGCGTCCGGCTCTTCT 793  
 QY 781 GGCTCCCGAGAAAGATCGCAACCTGGTAGGATCACACAGACTGGTCTGCTGGTGGTG 840  
 DB 794 GGCTCCCGAGAAAGATCGCAACCTGGTAGGATCACACAGACTGGTCTGCTGGTGGTG 853  
 QY 841 GCAGTCTTGGTCTGTGCTGGACTCCCATTCACATTCATTCATCTGCTGGTGGAGCTCTGGGG 900  
 DB 854 GCGGTTTTGCTGCTGTGCTGGACTCCCATTCACATTCATTCATCTGCTGGTGGAGCTCTGGGG 913  
 QY 901 AGCAGCTCCACAGACAGAGCTGCTCTCCAGCTATTACTTTCGATCGCCTTAGCTAT 960  
 DB 914 AGCAGCTCCACAGACAGAGCTGCTCTCCAGCTATTACTTTCGATCGCCTTAGCTAT 973  
 QY 961 ACCAAGTAGCTGAAATCCCATTTCTACGCTTTCTTGTGATGAAATTTCAAGCGGTGT 1020  
 DB 974 ACCAAGTAGCTGAAATCCCATTTCTACGCTTTCTTGTGATGAAATTTCAAGCGGTGT 1033  
 QY 1021 TTCCGGGACTTCTGCTTCCACTGAAGATGAGATGGAGCGGCGAGCAGCTAGCAGATC 1080  
 DB 1034 TTCCGGGACTTCTGCTTCCACTGAAGATGAGATGGAGCGGCGAGCAGCTAGCAGATC 1093  
 QY 1081 CGAATACAGTTTCAGATCTCTTACCTGAGGACATCGATGGATGAATAAACAGTA 1140  
 DB 1094 CGAATACAGTTTCAGATCTCTTACCTGAGGACATCGATGGATGAATAAACAGTA 1153  
 QY 1141 TGACTAGTCTGGGA 1154  
 DB 1154 TGACTAGTCTGGGA 1167

RESULT 13  
 ADI56615  
 ID ADI56615 standard; DNA; 1182 BP.  
 XX ADI56615;  
 AC ADI56615;  
 XX 22-APR-2004 (first entry)  
 DT Human polynucleotide probe #1417.  
 DE Human; probe; ss; receptor-like polypeptide; transducing polypeptide;  
 KW effector-like polypeptide; cancer; immunopathology; neuropathology;  
 KW drug development; toxicology; carcinogenicity;  
 KW signalling pathway polypeptide; adrenal gland; bladder; bone;  
 KW bone marrow; brain; breast; cervix; tumour; immunopathology; AIDS;  
 KW diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology;  
 KW dementia; amnesia; epilepsy; Alzheimer's disease; depression.  
 XX Homo sapiens.  
 OS US2004010136-A1.  
 PN 15-JAN-2004.  
 XX 26-NOV-2002; 2002US-00305720.  
 PF 30-JAN-1998; 98US-00016434.  
 PR (INCY-) INCYTE GENOMICS INC.  
 PA Au-Young J, Seilhamer JJ;  
 XX WPI; 2004-090520/09.  
 DR New composition comprising polynucleotide probes, useful as array  
 PT elements in a microarray for monitoring the expression of target  
 PT polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic

PT fragments.

PS Claim 6; SEQ ID NO 1417; 73pp; English.

XX  
CC The invention relates to a composition of polynucleotide probes  
CC comprising first polynucleotide probes comprising at least a portion of a  
CC gene encoding a receptor-like polypeptide, second polynucleotide probes  
CC comprising at least a portion of a gene encoding a transducing  
CC polypeptide and third polynucleotide probes comprising at least a portion  
CC of a gene encoding an effector-like polypeptide. The probes of the  
CC composition are useful as array elements in a microarray for monitoring  
CC the expression of target polynucleotides. The microarray is useful in the  
CC diagnosis and treatment of cancer, an immunopathology or a  
CC neuropathological. It can also be used for drug discovery and development,  
CC toxicological and carcinogenicity studies, forensics or pharmacogenomics.  
CC Microarrays can also be used for monitoring the progression of diseases  
CC that may be associated with the altered expression of signalling pathway  
CC polypeptides. The composition can also be used to purify a subpopulation  
CC of mRNAs, cDNAs, or genomic fragments in a sample. The expression profile  
CC is also useful for the diagnosis and treatment of cancer, e.g. cancers of  
CC the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix,  
CC an immunopathology, e.g. AIDS, diabetes, pancreatitis, osteoporosis or  
CC ulcerative colitis, or a neuropathology, e.g. dementia, amnesia,  
CC epilepsy, Alzheimer's disease or depression. This sequence represents a  
CC human polynucleotide probe of the invention. Note: The sequence data for  
CC this patent did not form part of the printed specification but was  
CC obtained in electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html.

XX  
SQ Sequence 1182 BP; 245 A; 345 C; 293 G; 299 T; 0 U; 0 Other;

Query Match 99.2%; Score 1144.4; DB 12; Length 1182;  
Best Local Similarity 99.5%; Pred. No. 2.3e-272;  
Matches 1148; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 61 TGCCTGCCCCCAACAGCAGCGCGCTGTTTCCCGCTGGCGCGAGCCCGCAGCAACGGC 120  
DB 74 TGCCTGCCCCCAACAGCAGCGCGCTGTTTCCCGCTGGCGCGAGCCCGCAGCAACGGC 133  
QY 121 AGCGCGGCTCGGAGGAGCGCAGCTGGAGCGCGCAGCATCTCCCGCGCCATCCCGGTC 180  
DB 134 AGCGCGGCTCGGAGGAGCGCAGCTGGAGCGCGCAGCATCTCCCGCGCCATCCCGGTC 193  
QY 181 ATCATCAGCGCGCTACTCGTAGTGTTCGCTGGGCTTGGTGGGCAACTCGCTGGTC 240  
DB 194 ATCATCAGCGCGCTACTCGTAGTGTTCGCTGGGCTTGGTGGGCAACTCGCTGGTC 253  
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QY 301 CTGCGCTTTGGCAGATGCTTTAGTTACTACACACCATGCGCTTTTCAGAGTACGGTCTACTTG 360  
DB 314 CTGCGCTTTGGCAGATGCTTTAGTTACTACACACCATGCGCTTTTCAGAGTACGGTCTACTTG 373  
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DB 374 ATGAATTTCTGGCTTTTGGGGATGTGCTGCGAAGATAGTAATTTCCATTGATTAATAC 433  
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DB 674 TGTGGGACCTCTTTCATGAAGATCTGCGTCTTTCATCTTTTGCCTTCCTGATCCCTGCTC 733  
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DB 734 ATCATCTCTGCTCTACACCCCTGATGATCTGCTGCTCTCAAGAGGCTCCGCTCTCTTCT 793  
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DB 794 GGCTCCCGAGAGAAGATCGCAACCTCGTAGGATCACCAGCTGGTCTCTGCTGCTG 853  
QY 841 GCAGTCTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
DB 854 GCGGTTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 913  
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DB 914 AGCAGCTCCACACAGCAGCTGCTCTCTCCAGCTATTACTTCTGATCGCTTCTAGGCTAT 973  
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DB 1034 TTCGGGACTTCTGCTTTTCCACTGAAGATGAGGATGAGCGGCGAGAGCCTAGCAGAGTC 1093  
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DB 1094 CGAATAACAGTTCAGGATCTGCTTACTCTGAGGACATCGATGGATGAATAAACACAGTA 1153  
QY 1141 TGACTAGTCTGGA 1154  
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AC AC  
XX AC  
DT 14-APR-1998 (first entry)  
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DE DE  
XX DE  
KW Selective target cell activation; G protein-coupled receptor; RASL;  
KW gene therapy; cell proliferation; kappa opioid receptor; human;  
KW transgenic animal; arrhythmia; bone disease; seizure;  
KW vascular contraction; disease model; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO9735478-A1.  
XX  
PD 02-OCT-1997.  
XX  
PF 25-MAR-1997; 97WO-US005334.  
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PR 26-MAR-1996; 96US-00622348.  
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PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Conklin BR;  
XX  
DR WPI; 1997-502739/46.





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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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(without alignments)  
8782.620 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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6: /cgn2\_6/ptodata/1/ina/backfiles.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1144.4	99.2	1182	US-09-016-434-1417	Sequence 1417, Ap
2	1141.4	98.9	1143	US-09-341-446B-1	Sequence 1, Appli
3	1140.4	98.8	1142	US-08-765-743-1	Sequence 1, Appli
4	1136.2	98.5	1284	US-09-341-446B-3	Sequence 3, Appli
5	1130.2	97.9	1143	US-09-826-509-542	Sequence 542, App
6	999.4	86.6	1275	US-09-341-446B-5	Sequence 5, Appli
7	994.6	86.2	1275	US-09-341-446B-7	Sequence 7, Appli
8	909.2	78.8	1408	US-09-214-904-5	Sequence 5, Appli
9	909.2	78.8	1410	US-08-147-592A-1	Sequence 1, Appli
10	869.6	75.4	1000	US-08-292-694A-1	Sequence 11, Appl
11	869.6	75.4	1000	US-08-147-592A-11	Sequence 11, Appl
12	869.6	75.4	1000	US-08-292-694A-11	Sequence 11, Appl
13	446.4	38.7	2135	US-08-430-286A-1	Sequence 1, Appli
14	444.8	38.5	1618	US-08-889-108-1	Sequence 1, Appli
15	444.8	38.5	1618	US-08-889-108-3	Sequence 3, Appli
16	444.8	38.5	1618	US-08-120-601B-1	Sequence 1, Appli
17	444.8	38.5	1618	US-08-120-601B-3	Sequence 3, Appli
18	444.8	38.5	1618	PCT-US94-10358-1	Sequence 1, Appli
19	444.8	38.5	1618	PCT-US94-10358-3	Sequence 3, Appli
20	433.2	37.5	1610	US-08-889-108-7	Sequence 7, Appli
21	433.2	37.5	1610	PCT-US94-10358-7	Sequence 7, Appli
22	433.2	37.5	2160	US-08-188-275A-1	Sequence 1, Appli
23	433.2	37.5	2162	US-09-351-198-1	Sequence 1, Appli
24	433.2	37.5	2162	US-09-113-426-1	Sequence 1, Appli
25	433.2	37.5	2162	US-09-016-434-1379	Sequence 1379, Ap
26	433.2	37.5	2162	US-09-355-709C-7	Sequence 7, Appli
27	430.8	37.3	1334	US-09-761-962A-3	Sequence 3, Appli

Sequence 11, Appl  
Sequence 1, Appli  
Sequence 16, Appl  
Sequence 9, Appli  
Sequence 10, Appl  
Sequence 546, App  
Sequence 544, App  
Sequence 1, Appli  
Sequence 4, Appli  
Sequence 15, Appl  
Sequence 15, Appl  
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Sequence 7, Appli  
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Sequence 3, Appli

## ALIGNMENTS

RESULT 1  
US-09-016-434-1417  
; Sequence 1417, Application US/09016434  
; Patent No. 6500938  
; GENERAL INFORMATION:  
; APPLICANT: Janice Au-Young  
; APPLICANT: Jeffrey J. Sellhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1490  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/016,434  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0002 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 1417:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1182 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: 9532059  
; US-09-016-434-1417

Query Match 99.2%; Score 1144.4; DB 4; Length 1182;  
Best Local Similarity 99.5%; Pred. No. 1.7e-283;

Matches 1148; Conservative 0; Mismatches 6; Indels 0; Gaps 0;									
QY	1	ATGGACTCCCGATCCAGATCTTCCGCGGGAGCGGGCCCTACTCTGCGCCCGAGCGCC	60						
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DB	74	TGCTGCCCGCCCAACAGCAGCGCTGGTTTCCGCGTGGCGGAGCCGACAGCAACCGC	133						
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QY	181	ATCATCAGCGGCTCTACTCCGTAGTGTTCGTGGGCTTGGTGGGCAACTCGCTGTC	240						
DB	194	ATCATCAGCGGCTCTACTCCGTAGTGTTCGTGGGCTTGGTGGGCAACTCGCTGTC	253						
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DB	254	ATGTTCTGTATCATCCGATACACAAAGATGAAGACAGCAACCAATTTACATATTAA	313						
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DB	314	CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTTCAGAGTACGGTCTACTTG	373						
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DB	374	ATGAATTCCTGGCTTTGGGATGTCTGTGCAAGATAGTATTTCCATTGATTACTAC	433						
QY	421	AACATGTTTACCAGATCTTCACTTGACCATGAGGTGACCGCTACATTGCCGTG	480						
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DB	614	GTGAGGAAAGACCTCGATGTCATTTAGTGTCTCTGAGTTCCTCAGATGATGACTACTCC	673						
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DB	674	TGTTGGGACCTCTTCATGAAGATCTGCTTTCATCTTTGCTTCTGATCCCTGTCCTC	733						
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DB	854	GCAGTCTTCTGCTGCTGGAATCCCATTCACATATTCATCTGTTGAGGCTCTGGGG	913						
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DB	914	AGCACCTCCACAGCAGAGCTCTCTCCAGCTATTACTTCTGCAATCCGCTTAGGCTAT	973						
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DB	974	ACCAACAGTAGTGCATCCCATTTCTTACGCTTTTCTTGATGAAATTTCAAGCGGTGT	1033						
QY	1021	TTCCGGGACTTCTGCTTTTCCATGAGATGAGGATGGAGCGGCGAGCAGTACAGAGTC	1080						
DB	1034	TTCCGGGACTTCTGCTTTTCCATGAGATGAGGATGGAGCGGCGAGCAGTACAGAGTC	1093						

QY	1081	CGAATACAGTTCAGATCTTCTTACCTGAGGACATCGATGGATGAATAAACAGTA	1140						
DB	1094	CGAATACAGTTCAGATCTTCTTACCTGAGGACATCGATGGATGAATAAACAGTA	1153						
QY	1141	TGACTAGTCGTGGA	1154						
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; Sequence 1, Application US/09341446B									
; Patent No. 6518480									
; GENERAL INFORMATION:									
; APPLICANT: Conklin, Bruce R.									
; TITLE OF INVENTION: Selective Target Cell Activation By									
; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated									
; FILE REFERENCE: UCAL-049CIP									
; CURRENT APPLICATION NUMBER: US/09/341,446B									
; CURRENT FILING DATE: 1999-12-20									
; PRIOR APPLICATION NUMBER: PCT/US97/05334									
; PRIOR FILING DATE: 1997-03-25									
; PRIOR APPLICATION NUMBER: US 08/622,348									
; PRIOR FILING DATE: 1996-03-26									
; NUMBER OF SEQ ID NOS: 12									
; SOFTWARE: FastSeq for Windows Version 4.0									
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; LENGTH: 1143									
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; ORGANISM: Homo sapiens									
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Best Local Similarity 99.9%; Pred. No. 9.6e-283;									
Matches 1142; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
QY	1	ATGGACTCCCGATCCAGATCTTCCGCGGGAGCGGGCCCTACTCTGCGCCCGAGCGCC	60						
DB	1	ATGGACTCCCGATCCAGATCTTCCGCGGGAGCGGGCCCTACTCTGCGCCCGAGCGCC	60						
QY	61	TGCTGCCCGCCCAACAGCAGCGCTGGTTTCCGCGTGGCGGAGCCGACAGCAACCGC	120						
DB	61	TGCTGCCCGCCCAACAGCAGCGCTGGTTTCCGCGTGGCGGAGCCGACAGCAACCGC	120						
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DB	121	AGCGCGGCTCGGAGCAGCGCGAGTGGAGCGCGCACATCTCCCGCGCCATCCGGTTC	180						
QY	181	ATCATCAGCGGCTCTACTCCGTAGTGTTCGTGGGCTTGGTGGGCAACTCGCTGTC	240						
DB	181	ATCATCAGCGGCTCTACTCCGTAGTGTTCGTGGGCTTGGTGGGCAACTCGCTGTC	240						
QY	241	ATGTTCTGTATCATCCGATACACAAAGATGAAGACAGCAACCAATTTACATATTAA	300						
DB	241	ATGTTCTGTATCATCCGATACACAAAGATGAAGACAGCAACCAATTTACATATTAA	300						
QY	301	CTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCTTTTCAGAGTACGGTCTACTTG	360						
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QY	361	ATGAATTCCTGGCTTTGGGATGTCTGTGCAAGATAGTATTTCCATTGATTACTAC	420						
DB	361	ATGAATTCCTGGCTTTGGGATGTCTGTGCAAGATAGTATTTCCATTGATTACTAC	420						
QY	421	AACATGTTTACCAGATCTTCACTTGACCATGAGGTGACCGCTACATTGCCGTG	480						
DB	421	AACATGTTTACCAGATCTTCACTTGACCATGAGGTGACCGCTACATTGCCGTG	480						
QY	481	TGCCACCCCGTGAAGCTTTGGACTTCCGCACACCCCTTGAAGCAAAAGATCATCAATATC	540						
DB	481	TGCCACCCCGTGAAGCTTTGGACTTCCGCACACCCCTTGAAGCAAAAGATCATCAATATC	540						





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QY 1021 TTCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGCGGAGAGCACTAGCAGAGTC 1080
Db |||
QY 1081 CGAAATACAGTTCAGGATCTGCTTACCTGAGGAGCATCGATGGGATGAATAAACAGTA 1140
Db |||
QY 1081 CGAAATACAGTTCAGGATCTGCTTACCTGAGGAGCATCGATGGGATGAATAAACAGTA 1140
Db |||
QY 1141 TG 1142
Db ||
QY 1141 TG 1142
Db ||
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## RESULT 4

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US-09-341-446B-3
; Sequence 3, Application US/09341446B
; Patent No. 6518480
; GENERAL INFORMATION:
; APPLICANT: Conklin, Bruce R.
; TITLE OF INVENTION: Selective Target Cell Activation By
; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated
; TITLE OF INVENTION: Superiorly By Synthetic Ligand
; FILE REFERENCES: UCAL-049CIP
; CURRENT FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US97/05334
; PRIOR FILING DATE: 1997-03-25
; PRIOR APPLICATION NUMBER: US 08/622,348
; PRIOR FILING DATE: 1996-03-26
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1284
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified KOR
US-09-341-446B-3
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Query Match 98.5%; Score 1136.2; DB 4; Length 1284;
Best Local Similarity 99.7%; Pred. No. 2.2e-281;
Matches 1138; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TGGACTCCCGGATCCAGATCTTCGGGGGAGCGGGCCCTACTCGGCCCGCAGCGCCT 61
Db 113 TCGACTCCCGGATCCAGATCTTCGGGGGAGCGGGCCCTACTCGGCCCGCAGCGCCT 172
QY 62 GCCTGCCCGCCAAACAGCAGCGCTGCTTCCCGGCTGGGCGGAGCCGACAGCAACGGCA 121
Db |||
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Db 173 GCCTGCCCGCCAAACAGCAGCGCTGCTTCCCGGCTGGGCGGAGCCCGACAGCAACGGCA 232
QY 173 GCCTGCCCGCCAAACAGCAGCGCTGCTTCCCGGCTGGGCGGAGCCCGACAGCAACGGCA 232
Db 181 GGGCGGCTCGGAGAGCGGAGCTGGAGCCCGCGACATCTCCCGGCGCATCCCGGTCA 181
QY 181 GGGCGGCTCGGAGAGCGGAGCTGGAGCCCGCGACATCTCCCGGCGCATCCCGGTCA 181
Db 223 GGGCGGCTCGGAGAGCGGAGCTGGAGCCCGCGACATCTCCCGGCGCATCCCGGTCA 292
QY 223 GGGCGGCTCGGAGAGCGGAGCTGGAGCCCGCGACATCTCCCGGCGCATCCCGGTCA 292
Db 241 TCATCAGCGCGGTCTACTCCGCTAGTGTTCGTCGTCGGGCTTGGTGGGCAACTCGCTGGTCA 241
QY 241 TCATCAGCGCGGTCTACTCCGCTAGTGTTCGTCGTCGGGCTTGGTGGGCAACTCGCTGGTCA 241
Db 352 TCATCAGCGCGGTCTACTCCGCTAGTGTTCGTCGTCGGGCTTGGTGGGCAACTCGCTGGTCA 352
QY 352 TCATCAGCGCGGTCTACTCCGCTAGTGTTCGTCGTCGGGCTTGGTGGGCAACTCGCTGGTCA 352
Db 301 TGTTCGTGATCATCCGATACACAAAGATGAAGAGAGCAAGCAACCAATTTACATTTAAACC 301
QY 301 TGTTCGTGATCATCCGATACACAAAGATGAAGAGAGCAAGCAACCAATTTACATTTAAACC 301
Db 412 TGTTCGTGATCATCCGATACACAAAGATGAAGAGAGCAAGCAACCAATTTACATTTAAACC 412
QY 412 TGTTCGTGATCATCCGATACACAAAGATGAAGAGAGCAAGCAACCAATTTACATTTAAACC 412
Db 361 TGGCTTTGGCAGATCGTTTGTAGTTACTACCAACATGCCCTTTTCAGAGTAGCGTCTACTGA 361
QY 361 TGGCTTTGGCAGATCGTTTGTAGTTACTACCAACATGCCCTTTTCAGAGTAGCGTCTACTGA 361
Db 472 TGGCTTTGGCAGATCGTTTGTAGTTACTACCAACATGCCCTTTTCAGAGTAGCGTCTACTGA 472
QY 472 TGGCTTTGGCAGATCGTTTGTAGTTACTACCAACATGCCCTTTTCAGAGTAGCGTCTACTGA 472
Db 421 TGAATTTCTTGGGCTTTTGGGATGTGCTGTGCAAGATAGTAAATTTCCATTTGATTACTACA 421
QY 421 TGAATTTCTTGGGCTTTTGGGATGTGCTGTGCAAGATAGTAAATTTCCATTTGATTACTACA 421
Db 532 TGAATTTCTTGGGCTTTTGGGATGTGCTGTGCAAGATAGTAAATTTCCATTTGATTACTACA 532
QY 532 TGAATTTCTTGGGCTTTTGGGATGTGCTGTGCAAGATAGTAAATTTCCATTTGATTACTACA 532
Db 481 ACATGTTACCAAGATCTTACCTTGAACATGATGAGCGTGAGCGCTACATTTGCCGTGT 481
QY 481 ACATGTTACCAAGATCTTACCTTGAACATGATGAGCGTGAGCGCTACATTTGCCGTGT 481
Db 592 ACATGTTACCAAGATCTTACCTTGAACATGATGAGCGTGAGCGCTACATTTGCCGTGT 592
QY 592 ACATGTTACCAAGATCTTACCTTGAACATGATGAGCGTGAGCGCTACATTTGCCGTGT 592
Db 541 GGCACCGGCTGAAGGCTTTGGGATTTCCGACACCTTGAAGGCAAGATCATCAATATCT 541
QY 541 GGCACCGGCTGAAGGCTTTGGGATTTCCGACACCTTGAAGGCAAGATCATCAATATCT 541
Db 652 GGCACCGGCTGAAGGCTTTGGGATTTCCGACACCTTGAAGGCAAGATCATCAATATCT 652
QY 652 GGCACCGGCTGAAGGCTTTGGGATTTCCGACACCTTGAAGGCAAGATCATCAATATCT 652
Db 601 GCATCTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 601
QY 601 GCATCTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 601
Db 712 GCATCTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 712
QY 712 GCATCTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 712
Db 661 TCAGGAGAGACCTCGATGTCTTGGATGTCTTGGATGTCTTGGATGTCTTGGATGTCTTGGAT 661
QY 661 TCAGGAGAGACCTCGATGTCTTGGATGTCTTGGATGTCTTGGATGTCTTGGATGTCTTGGAT 661
Db 772 TCAGGAGAGACCTCGATGTCTTGGATGTCTTGGATGTCTTGGATGTCTTGGATGTCTTGGAT 772
QY 772 TCAGGAGAGACCTCGATGTCTTGGATGTCTTGGATGTCTTGGATGTCTTGGATGTCTTGGAT 772
Db 721 GGTGGGACCTTTCATGAAGATCTGCGTCTTCAAGAGCGTCCGCTCTCTTCTG 721
QY 721 GGTGGGACCTTTCATGAAGATCTGCGTCTTCAAGAGCGTCCGCTCTCTTCTG 721
Db 832 GGTGGGACCTTTCATGAAGATCTGCGTCTTCAAGAGCGTCCGCTCTCTTCTG 832
QY 832 GGTGGGACCTTTCATGAAGATCTGCGTCTTCAAGAGCGTCCGCTCTCTTCTG 832
Db 781 TCATCATCTGCTGTACACCTCTGATGATCTTCAAGAGCGTCCGCTCTCTTCTG 781
QY 781 TCATCATCTGCTGTACACCTCTGATGATCTTCAAGAGCGTCCGCTCTCTTCTG 781
Db 892 TCATCATCTGCTGTACACCTCTGATGATCTTCAAGAGCGTCCGCTCTCTTCTG 892
QY 892 TCATCATCTGCTGTACACCTCTGATGATCTTCAAGAGCGTCCGCTCTCTTCTG 892
Db 841 GCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACAGACTGCTGCTGCTGCTGCTGCTG 841
QY 841 GCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACAGACTGCTGCTGCTGCTGCTGCTG 841
Db 952 GCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACAGACTGCTGCTGCTGCTGCTGCTG 952
QY 952 GCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACAGACTGCTGCTGCTGCTGCTGCTG 952
Db 901 CAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 901
QY 901 CAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 901
Db 1012 CAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1012
QY 1012 CAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1012
Db 961 GCACCTTCCACAGCAGCTGCTCTCTCCAGCTATTACTTCTGCACTCCCTTAGGCTATA 961
QY 961 GCACCTTCCACAGCAGCTGCTCTCTCCAGCTATTACTTCTGCACTCCCTTAGGCTATA 961
Db 1072 GCACCTTCCACAGCAGCTGCTCTCTCCAGCTATTACTTCTGCACTCCCTTAGGCTATA 1072
QY 1072 GCACCTTCCACAGCAGCTGCTCTCTCCAGCTATTACTTCTGCACTCCCTTAGGCTATA 1072
Db 1021 CCAACAGTAGCTGAATCCCATTTCTAGCGCTTTCTTGAATGAAATTTCAAGCGGTGT 1021
QY 1021 CCAACAGTAGCTGAATCCCATTTCTAGCGCTTTCTTGAATGAAATTTCAAGCGGTGT 1021
Db 1132 CCAACAGTAGCTGAATCCCATTTCTAGCGCTTTCTTGAATGAAATTTCAAGCGGTGT 1132
QY 1132 CCAACAGTAGCTGAATCCCATTTCTAGCGCTTTCTTGAATGAAATTTCAAGCGGTGT 1132
Db 1081 TCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGCGGAGAGCACTAGCAGAGTCC 1081
QY 1081 TCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGCGGAGAGCACTAGCAGAGTCC 1081
Db 1192 TCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGCGGAGAGCACTAGCAGAGTCC 1192
QY 1192 TCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGAGCGGAGAGCACTAGCAGAGTCC 1192
Db 1141 GAAATACAGTTCAGGATCTGCTTACCTGAGGAGCATCGATGGATGAATAAACAGTAT 1141
QY 1141 GAAATACAGTTCAGGATCTGCTTACCTGAGGAGCATCGATGGATGAATAAACAGTAT 1141
Db 1252 GAAATACAGTTCAGGATCTGCTTACCTGAGGAGCATCGATGGATGAATAAACAGTAT 1252
QY 1252 GAAATACAGTTCAGGATCTGCTTACCTGAGGAGCATCGATGGATGAATAAACAGTAT 1252
Db 1142 G 1142
QY 1142 G 1142
Db 1253 G 1253
QY 1253 G 1253
Db 1253 G 1253
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	Query Match	86.6%;	Score 999.4;	DB 4;	Length 1275;
	Best Local Similarity	93.0%;	Pred. No. 2.6e-246;		
	Matches 1061;	Conservative	0;	Mismatches 71;	Indels 9; Gaps 1;
Qy	2	TGGACTCCCGATCCAGATCTTCCGGGGAGCCGGGGCCCTACCTGCGCCCGAGCGCCT	61		
Db	113	TGACTCTCCCGATCCAGATCTTCCGGGGAGCCGGGGCCCTACCTGCGCCCGAGCGCCT	172		

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QY 62 GCCTGCCCCCAACAGCAGCGCTGTTTCCCGGCTGGCCGAGCCGACAGCAACGGCA 121
Db 173 GCCTGCCCCCAACAGCAGCGCTGTTTCCCGGCTGGCCGAGCCGACAGCAACGGCA 232
QY 122 GCGCCGGCTCGGAGGACGCGAGCTGGAGCCCGCGCACATCTCCCGGCCATCCCGGTCA 181
Db 233 GCGCCGGCTCGGAGGACGCGAGCTGGAGCCCGCGCACATCTCCCGGCCATCCCGGTCA 292
QY 182 TCATCAGCGGCTTACTCGGTAGTGTTCGTGGGCTTGGTGGCAACTCGCTGGTCA 241
Db 293 TCATCAGCGGCTTACTCGGTAGTGTTCGTGGGCTTGGTGGCAACTCGCTGGTCA 352
QY 242 TGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 301
Db 353 TGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 412
QY 302 TGGCTTTGGAGATGCTTTAGTTTATACAAACATGCTTTCAGAGTACGGTCTACTTGA 361
Db 413 TGGCTTTGGAGATGCTTTAGTTTATACAAACATGCTTTCAGAGTACGGTCTACTTGA 472
QY 362 TGAATTCCTGGCCCTTTTGGGATGCTGTGCAAGATAGTATTTCCATTTGATTACTACA 421
Db 473 TGAATTCCTGGCCCTTTTGGGATGCTGTGCAAGATAGTATTTCCATTTGATTACTACA 532
QY 422 ACATGTTTCCAGCATCTTCCACCTTGACCATGATGAGCGTGGACCGCTACATTTGCCGTGT 481
Db 533 ACATGTTTCCAGCATCTTCCACCTTGACCATGATGAGCGTGGACCGCTACATTTGCCGTGT 592
QY 482 GCCACCCCGTGAAGGCTTTGGATCTCCGACACCTTTGAAGGCAAAAGATCATCAATCT 541
Db 593 GCCACCCCGTGAAGGCTTTGGATCTCCGACACCTTTGAAGGCAAAAGATCATCAATCT 652
QY 542 GCATCTGGCTGCTGCTGATCTGTTGGATCTCTGCAATAGTCCCTTGGAGGACCAAG 601
Db 653 GCATCTGGCTGCTGCTGATCTGTTGGATCTCTGCAATAGTCCCTTGGAGGACCAAG 712
QY 602 TCAGGGAAGACGTCGATGTCAATGAGTGTCTTTCGAGTTCCTGAGATGCCAGATGATCTCCT 661
Db 713 CCAGGATGGAGCAGTGGTATGCAACGCTCCAGTTCCTGAGGCTTCCAGGCTTCCAGGCT 763
QY 662 GGTGGGACCTTTCATGAAGATCTGGGCTTTCATCTTTGGCTTTCGATGATCCCTGCTCA 721
Db 764 ACTGGGACACTGTGACCAAGATCTGGGCTTTCATCTTTGGCTTTCGATGATCCCTGCTCA 823
QY 722 TCATCATCTGCTGCTACACCTGATCTGCTGCTGCTCAAGAGCTCCGCTCTCTTTCTG 781
Db 824 TCATCATCTGCTGCTACACCTGATCTGCTGCTGCTCAAGAGCTCCGCTCTCTTTCTG 883
QY 782 GCTCCCGAGAGAAAGATCGCAACCTGCTGAGGATCAACAGATGCTGCTGCTGCTGCTG 841
Db 884 GCTCCCGAGAGAAAGATCGCAACCTGCTGAGGATCAACAGATGCTGCTGCTGCTGCTG 943
QY 842 CAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 901
Db 944 CAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1003
QY 902 GCACCTCCCAACAGCAGCTGCTCTCCAGCTATTACTTCTGATCGCTTAGGCTTATA 961
Db 1004 GCACCTCCCAACAGCAGCTGCTCTCCAGCTATTACTTCTGATCGCTTAGGCTTATA 1063
QY 962 CCAACAGTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1021
Db 1064 CCAACAGTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1123
QY 1022 TCCGGGACTTCTGCTTTCATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1081
Db 1124 TCCGGGACTTCTGCTTTCATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1183
QY 1082 GAAATACAGTTCAGGATCTGCTTACCTGAGGACATCGATGGATGGAATGGAATGGAAT 1141
Db 1184 GAAATACAGTTCAGGATCTGCTTACCTGAGGACATCGATGGATGGAATGGAATGGAAT 1243
QY 1142 G 1142

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Db 1244 G 1244

RESULT 7

US-09-341-446B-7

; Sequence 7, Application US/09341446B

; Patent No. 6518480

; GENERAL INFORMATION:

; APPLICANT: Conklin, Bruce R.

; TITLE OF INVENTION: Selective Target Cell Activation By

; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated

; FILE REFERENCE: UCAL-049CIP

; CURRENT APPLICATION NUMBER: US/09/341,446B

; CURRENT FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US97/05334

; PRIOR FILING DATE: 1997-03-25

; PRIOR APPLICATION NUMBER: US 08/622,348

; PRIOR FILING DATE: 1996-03-26

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7

; LENGTH: 1275

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: RASSL OR2

; US-09-341-446B-7

Query Match

Best Local Similarity 86.2%; Score 994.6; DB 4; Length 1275;

Matches 1058; Conservative 0; Mismatches 74; Indels 9; Gaps 1;

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QY 2 TCGACTCCCGGATCCAGATCTTCCGGGGAGCGGGCCCTTACCTGCGCCCGGCGCCT 61
Db 113 TCGACTCCCGGATCCAGATCTTCCGGGGAGCGGGCCCTTACCTGCGCCCGGCGCCT 172
QY 62 GCTGCGCCCGGATCCAGATCTTCCGGGGAGCGGGCCCTTACCTGCGCCCGGCGCCT 121
Db 173 GCTGCGCCCGGATCCAGATCTTCCGGGGAGCGGGCCCTTACCTGCGCCCGGCGCCT 232
QY 122 GCGCGGCTCGGAGGACGCGAGCTGGAGCCCGCGGACATCTCCCGGCGCATCCCGGTCA 181
Db 233 GCGCGGCTCGGAGGACGCGAGCTGGAGCCCGCGGACATCTCCCGGCGCATCCCGGTCA 292
QY 182 TCATCAGCGGCTTACTCTCGGTAGTGTTCGTGCTGGGCTTGGTGGGCAACTCGCTGCTCA 241
Db 293 TCATCAGCGGCTTACTCTCGGTAGTGTTCGTGCTGGGCTTGGTGGGCAACTCGCTGCTCA 352
QY 242 TGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 301
Db 353 TGTTCGTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAC 412
QY 302 TGGCTTTGGAGATGCTTTAGTTTATACAAACATGCTTTCAGAGTACGGTCTACTTGA 361
Db 413 TGGCTTTGGAGATGCTTTAGTTTATACAAACATGCTTTCAGAGTACGGTCTACTTGA 472
QY 362 TGAATTCCTGGCCCTTTTGGGATGCTGCTGCAAGATAGTATTTCCATTTGATTACTACA 421
Db 473 TGAATTCCTGGCCCTTTTGGGATGCTGCTGCAAGATAGTATTTCCATTTGATTACTACA 532
QY 422 ACATGTTTCCAGCATCTTCCACCTTGACCATGATGAGCGTGGACCGCTACATTTGCCGTGT 481
Db 533 ACATGTTTCCAGCATCTTCCACCTTGACCATGATGAGCGTGGACCGCTACATTTGCCGTGT 592
QY 482 GCCACCCCGTGAAGGCTTTGGATCTCCGACACCTTTGAAGGCAAAAGATCATCAATCT 541
Db 593 GCCACCCCGTGAAGGCTTTGGATCTCCGACACCTTTGAAGGCAAAAGATCATCAATCT 652
QY 542 GCATCTGGCTGCTGCTGATCTGTTGGATCTCTGCAATAGTCCCTTGGAGGACCAAG 601
Db 653 GCATCTGGCTGCTGCTGATCTGTTGGATCTCTGCAATAGTCCCTTGGAGGACCAAG 712

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Db 1144 ACCAACAGCAGCCGTAATCCTGTTCTATGCCCTTTCTGGATGAAATTTCAAGCGGTGT 1203  
 Qy 1021 TTCCGGGACTTCTGCTTTTCCACTGAAGATCAGAGTGGAGCGGCAGAGCACTAGCAGATC 1080  
 Db 1204 TTTAGGGACTTCTGCTTTCCCTATTAGATGCGAATGGAGCGCCAGAGCACCAATAGAGTT 1263  
 Qy 1081 CGAAATACAGTTTCAAGATCCTGCTTACCTTGAGGACATCGATGGGATGAATAAACAGTA 1140  
 Db 1264 AGAAACAGATTTCAGATCCTGCTTCCATGAGAGATGTGGAGGGATGAATAAGCCAGTA 1323  
 Qy 1141 TGAATAGTCGTGGA 1154  
 Db 1324 TGAATAGTCGTGGA 1337

RESULT 9

US-08-147-592A-1  
 ; Sequence 1, Application US/08147592A  
 ; Patent No. 6096513  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bell, Graeme I  
 ; APPLICANT: Kelsine, Terry  
 ; APPLICANT: Yasuda, Kazuki  
 ; TITLE OF INVENTION: Opioid Receptor Genes,  
 ; TITLE OF INVENTION: Compositions and Methods  
 ; NUMBER OF SEQUENCES: 43  
 ; CORRESPONDENCE ADDRESSES:  
 ; ADDRESSEE: Arnold, White & Durkee  
 ; STREET: P.O. Box 4433  
 ; CITY: Houston  
 ; STATE: Texas  
 ; COUNTRY: United States of America  
 ; ZIP: 72210  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/147,592A  
 ; FILING DATE: 05-NOV-1993  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/100,694  
 ; FILING DATE: 30-JUL-1993  
 ; CLASSIFICATION: 435  
 ; APPLICATION NUMBER: 08/066,296  
 ; FILING DATE: 20-MAY-1993  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Wilson, Mark B.  
 ; REGISTRATION NUMBER: 37,259  
 ; REFERENCE/DOCKET NUMBER: ARCD:105  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (512) 418-3000  
 ; TELEFAX: (512) 474-7577  
 ; TELEX: N/A  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1410 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 186..1325  
 ; US-08-147-592A-1

Query Match 78.8%; Score 909.2; DB 3; Length 1410;  
 Best Local Similarity 86.7%; Pred. No. 3.7e-223;  
 Matches 1001; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

Qy 1 ATGGACTCCCGATCCAGATCTTCCGCGGGAGCGGGCCCTTACTGTGCGCCCGAGCGCC 60  
 Db 186 ATGGAGTCCCGATCCAGATCTTCCGAGGAGATCCAGGCGCTTACCTGTCTCTCCAGTGT 245  
 Qy 61 TGCCTGCCCGCCAAACAGAGCGCCTTGGTTCCGGCTGGGCGGAGCCCGAGAGCAACGCG 120  
 Db 246 TGCCTTCTCCCGAAACAGAGCGCTTGGTTCCCGAACTGGGCGAATCCGACAGTAATGGC 305  
 Qy 121 AGCGCGGCTCGAGAGCGCGCAGCTGGAGCGCGGCACATCTCCCGGCCCATCCCGGTC 180  
 Db 306 AGTGTGGGCTCAGAGGATCAGCAGCTGGAGTCCGCGCACTCTCCGCGCATCCCTGTT 365  
 Qy 181 ATCATCAGCGCGTCTACTCCGTTAGTGTCTGCTGGGCTTGGTGGGCAATCTCGTGGTC 240  
 Db 366 ATCATCAGCGCTGTCTACTCTGTTGTTGTTGGGCTTAGTGGGCAATCTCTGGTC 425  
 Qy 241 ATGTTGCTGATCATCCGATACAAAGATGAAGAGAGCAACCAACATTTACATATTTAAC 300  
 Db 426 ATGTTTGTTCATCCGATACAGAGATGAAGAGCGCAACCAACATCTACATATTTAAC 485  
 Qy 301 CTGGCTTTGGCAGATGCTTTTACTACTACCACTGCCCCCTTTTCCAGAGTACGGTCTACTTG 360  
 Db 486 CTGGCTTTGGCAGATGCTTTTGGTTACTACCACTATGCCCTTTTCCAGAGTCTGTCTACTTG 545  
 Qy 361 ATGAATTCCTGGCCTTTTGGGATGTCTGTGCAAGATAGTAATTTCCATTAATTAATAC 420  
 Db 546 ATGAATTCCTGGCCTTTTGGGATGTCTGTGCAAGATAGTAATTTCCATTAATTAATAC 605  
 Qy 421 AACATGTTTCCAGAGATCTTCACTTGCATGATGAGCGTGGACCGCTACATTTGCCGTG 480  
 Db 606 AACATGTTTACCAGCATATTTCACTTGCATGATGAGCGTGGACCGCTACATTTGCCGTG 665  
 Qy 481 TGCCACCGCTGAAAGCTTTTGGACTTCCGCACACCTTGAAGGCAAGATCATCAATATC 540  
 Db 666 TGCCACCGCTGAAAGCTTTTGGACTTCCGCACACCTTGAAGGCAAGATCATCAATATC 725  
 Qy 541 TGCACTCTGCTGCTGTGTCATCTGTGTCATCTCTGCAATAGTCTCTGGAGGACACAAA 600  
 Db 726 TGCACTTGGCTCTTGGCATCATCTGTGTTGTTATATCAGCGATAGTCTTGGAGGACACAAA 785  
 Qy 601 GTCAGGAGAGCTGATGTCATTGATGTCCTTTCAGTTCCTGAGTCCAGATGATGATCTCC 660  
 Db 786 GTCAGGAGAGCTGATGTCATTGATGTCCTTTCAGTTCCTGAGTCCAGATGATGATCTCC 845  
 Qy 661 TGCTGGGACCTCTTCATGAAGATCTGCTGCTTTCATCTTTCGCTTTCGATGATGATGAT 720  
 Db 846 TGCTGGGATCTCTTCATGAAGATCTGCTGCTTTCGCTTTCGATGATGATGATGATGAT 905  
 Qy 721 ATCATCATCTGCTGTCTACACCTGATGATCTGCTGCTTCAAGAGCGTCCGGCTCTTTCT 780  
 Db 906 ATCATCATCTGCTGTCTACACCTGATGATCTGCTGCTTCAAGAGTGTCCGGCTCTCTGT 965  
 Qy 781 GGTCTCCGAGAGAGATCGAACCTGCTGATGATGATGATGATGATGATGATGATGATGATG 840  
 Db 966 GGTCTCCGAGAGAGATCGAACCTGCTGATGATGATGATGATGATGATGATGATGATGAT 1025  
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 Db 1026 GCAGTCTTCTGCTGTGGAATCCCATTCATATTCATCTGCTGCTGAGGCTCTGCGGA 1085  
 Qy 901 AGCACCTCCACAGCAGCTGCTCTCCAGTATTAATTTCTGCAATGCCCTTAGGCTAT 960  
 Db 1086 AGCACCTCCACAGCAGCTGCTCTCCAGTATTAATTTCTGCAATGCCCTTAGGCTAT 1145  
 Qy 961 ACCACAGTAGCTGATCCCATTCCTAGCGCTTCTTGTGATGAAATTTCAAGCGGTGT 1020  
 Db 1146 ACCACAGTAGCTGATCCCATTCCTAGCGCTTCTTGTGATGAAATTTCAAGCGGTGT 1205  
 Qy 1021 TTCCCGGACTTCTGCTTTCCACTGAAGATGAGGAGCGGCGAGAGCACTAGCAGATC 1080  
 Db 1206 TTTAGGAGCTTCTGCTTCCCTATTAGATGCGAATGGAGCGCCAGAGCAACATAGATT 1265  
 Qy 1081 CGAAATACAGTTTCAAGATCCTGCTTACCTAGGAGCATCGATGGGATGAATAAACAGTA 1140





QY 1141 TGACTAGTCGTGGA 1154  
Db 1326 TGACTAGTCGTGGA 1339

RESULT 11

US-08-147-592A-11  
; Sequence 11, Application US/08147592A  
; Patent No. 6096513  
; GENERAL INFORMATION:  
; APPLICANT: Bell, Graeme I  
; APPLICANT: Reisine, Terry  
; APPLICANT: Yasuda, Kazuki  
; APPLICANT: Yasuda, Kazuki  
; TITLE OF INVENTION: Opioid Receptor Genes,  
; TITLE OF INVENTION: Compositions and Methods  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States of America  
; ZIP: 72210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/147,592A  
; FILING DATE: 05-NOV-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/100,694  
; FILING DATE: 30-JUL-1993  
; CLASSIFICATION: 435  
; APPLICATION NUMBER: 08/066,296  
; FILING DATE: 20-MAY-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wilson, Mark B.  
; REGISTRATION NUMBER: 37,259  
; REFERENCE/DOCKET NUMBER: ARCD:105  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 474-7577  
; TELEX: N/A  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1000 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; FEATURE:  
; NAME/KEY: N  
; LOCATION: 607-608, 642-643, 896, 906  
; IDENTIFICATION METHOD: N = A, C, G or T  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 102...986  
; FEATURE:  
; NAME/KEY: Xaa  
; LOCATION: 169, 181, 265, 269  
; IDENTIFICATION METHOD: Xaa = unknown  
US-08-147-592A-11

Query Match 75.4%; Score 869.6; DB 3; Length 1000;  
Best Local Similarity 97.5%; Pred. No. 4.5e-213;  
Matches 891; Conservative 0; Mismatches 20; Indels 3; Gaps 1;  
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87	TTCTTTTCTTTTAGATACACAAAGATGAAGACAGCAACCAATTTACATATTTAACTG	146
304	GCTTTGGCAGATGCTTTAGTTACTACACACCTGCTTTCAGAGTACGCTTACTTGATG	363
147	GCTTTGGCAGATGCTTTAGTTACTACACACCTGCTTTCAGAGTACGCTTACTTGATG	206
364	AATTCCTGGCCTTTTGGGATGCTGTGCAAGATAGTAATTTCCATTGATTACTACAC	423
207	AATTCCTGGCCTTTTGGGATGCTGTGCAAGATAGTAATTTCCATTGATTACTACAC	266
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267	ATGTTTACCAGCATCTTCACTTGACCATGATGAGCGTGGACCGGTACATTCCTGTCG	326
484	CACCCCGTGAAGGCTTTGGACTTTCGACACCTTTGAAGGCAAGATCATCAATCTCG	543
327	CACCCCGTGAAGGCTTTGGACTTTCGACACCTTTGAAGGCAAGATCATCAATCTCG	386
544	ATCTGGCTGCTGCTGCTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGACCAAAATC	603
387	ATCTGGCTGCTGCTGCTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGACCAAAATC	446
604	AGGGAAGAGCTGATGTCATGAGTGCTCTTGGAGTTCCTGAGATGATGATCTCTGTCG	663
447	AGGGAAGAGCTGATGTCATGAGTGCTCTTGGAGTTCCTGAGATGATGATCTCTGTCG	506
664	TGGGACCTTTCATGAGATGCTGCTTTCATCTTGGCTTTCGCTGATGATCTCTGTCG	723
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724	ATCATGCTGCTGCTACACCTGATGATCTGCTGCTCTCAAGAGGCTCCGGCTCTCTGTCG	783
567	ATCATGCTGCTGCTACACCTGATGATCTGCTGCTCTCAAGAGGCTCCGGCTCTCTGTCG	626
784	TCCGAGAGAAAGATGCGAACCTGCTGAGATGATGATGATGATGATGATGATGATGATG	843
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844	GTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	903
687	GTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	746
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807	AACAGTAGCTGAATCCCATTTCTACGCTTTTCTGATGATGATGATGATGATGATGATGATG	866
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867	CGGGACTTCTGCTTTCCTGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG	926
1084	AATACAGTTTCAAGTCTCTTACCTTACCTGAGGACATCGATG--GATGAATAAACAGTA	1140
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RESULT 12  
US-08-292-694A-11  
; Sequence 11, Application US/08292694A  
; Patent No. 6319686  
; GENERAL INFORMATION:  
; APPLICANT: BELL, GRAEME  
; APPLICANT: REISINE, TERRY  
; APPLICANT: YASUDA, KAZUKI  
; TITLE OF INVENTION: OPIOID RECEPTORS: COMPOSITIONS AND METHODS

NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P. O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/292,694A  
FILING DATE: August 19, 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/066,296  
FILING DATE: 20 May 1993  
CLASSIFICATION: 435  
APPLICATION NUMBER: 08/100,694  
FILING DATE: 30 July, 1993  
CLASSIFICATION: 435  
APPLICATION NUMBER: 08/147,592  
FILING DATE: 5 No. 6319686member 1993  
CLASSIFICATION: 435  
APPLICATION NUMBER: PCT/US94/05747  
FILING DATE: 20 May 1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MARK B. WILSON  
REGISTRATION NUMBER: 37,259  
REFERENCE/DOCKET NUMBER: ARCD:140/WIM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (713) 789-2679  
TELEX: 79-0924  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1000 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: N  
LOCATION: 607-608, 642-643, 896, 906  
IDENTIFICATION METHOD: N = A, C, G or T  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 102..986  
FEATURE:  
NAME/KEY: Xaa  
LOCATION: 169, 181, 265, 269  
IDENTIFICATION METHOD: Xaa = unknown  
US-08-292-694A-11

Query Match 75.4%; Score 869.6; DB 3; Length 1000;  
Best Local Similarity 97.5%; Pred. No. 4.5e-213;  
Matches 891; Conservative 0; Mismatches 20; Indels 3; Gaps 1;  
Qy 244 TTCGTGATCCGATACACAAAGATGAAGACAGACCAACATTTTACATATTTAACTG 303  
Db 87 TTCCTTTCTTTAGATACACAAAGATGAAGACAGACCAACATTTACATATTTAACTG 146  
Qy 304 GCTTTGGCAGATGCTTTAGTTACTACAAACCATGCCCTTTTCAGAGTACGGTCTACTTGATG 363  
Db 147 GCTTTGGCAGATGCTTTAGTTACTACAAACCATGCCCTTTTCAGAGTACGGTCTACTTGATG 206  
Qy 364 AATTCCTGGCCCTTTGGGGATGCTGTGCAAGATAGTAATTTCCATGATTACTACAAC 423  
Db 207 AATTCCTGGCCCTTTGGGGATGCTGTGCAAGATAGTAATTTCCATGATTACTACAAC 266

Qy 424 ATGTTCCACGACATCTTCAACCTTGACCATGATGAGCGTGGACCGCTACATTCGCGTGTGC 483  
Db 267 ATGTTCCACGACATCTTCAACCTTGACCATGATGAGCGTGGACCGCTACATTCGCGTGTGC 326  
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Db 327 CACCCCGTGAAGGCTTTGGACTTCGGCACACCCCTTGAAGGCAAGAGATCATCAATATCTGC 386  
Qy 544 ATCTGGCTGCTGCTGATCTGATCTGTTGGGATCTCTCAATAGTCTTGGAGGACCAAGTTC 603  
Db 387 ATCTGGCTGCTGCTGATCTGTTGGGATCTCTGCAATAGTCTTGGAGGACCAAGTTC 446  
Qy 604 AGGGAAGACGTCGATGTCAATTGAGTGTCTCTTGAGGTTCCAGAGTATGACTACTCTCTGG 663  
Db 447 AGGGAAGGTCGATGTCAATTGAGTGTCTCTTGAGGTTCCAGAGTATGACTACTCTCTGG 506  
Qy 664 TGGGACCTCTTCATGAAGATCTGGTCTTCACTTTGGCTTCGTGATCCCTGTCTCTCATC 723  
Db 507 TGGGACCTCTTCATGAAGATCTGGTCTTCACTTTGGCTTCGTGATCCCTGTCTCTCATC 566  
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Db 567 ATCATGCTGCTACACCCCTGATGATCTGCGTCTCAAGANNNGTCCGCTCTCTTCTGCGC 626  
Qy 784 TCCCGAGAGAAAGATCGCAACCTCGTAGGATCACAGACTGGTCTCTGGTGGTGGTGGCA 843  
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Qy 844 GTCTTCGTGCTGCTGGACTCCCATTCACATATTCATCTCTGGTGGAGGCTCTGGGGAGC 903  
Db 687 GTCTTCGTGCTGCTGGACTCCCATTCACATATTCATCTCTGGTGGAGGCTCTGGGGAGC 746  
Qy 904 ACCTCCACAGCAGAGCTGCTCTCCAGCTATTACTCTGCACTGCTTAGGCTATACC 963  
Db 747 ACCTCCACAGCAGAGCTGCTCTCCAGCTATTACTCTGCACTGCTTAGGCTATACC 806  
Qy 964 AACAGTAGCCTGAATCCCATTTCTACGCTCTTCTGATGAAAATTTCAAGCGGTGTTTC 1023  
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Qy 1024 CGGACTTCTGCTTTCCACTGAAGATGAGGATGAGGCGGAGAGACACTAGCAGAGTCCGA 1083  
Db 867 CGGACTTCTGCTTTCCACTGAAGATGAGGATGAGGCGGAGAGACACTAGCAGAGTCCGA 926  
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Db 987 TGACTAGTCTGGA 1000

RESULT 13  
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; Sequence 1, Application US/08430286A  
; Patent No. 6225080  
; GENERAL INFORMATION:  
; APPLICANT: Uhl, George R.  
; APPLICANT: Eppler, C. Mark  
; APPLICANT: Wang, Jai-Bel  
; TITLE OF INVENTION: Mu-Subtype Opioid Receptor  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Darby & Darby PC  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: US  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk



RESULT 15

US-08-889-108-3

Sequence 3, Application US/08889108

Patent No. 6103492

GENERAL INFORMATION:

APPLICANT: Yu, Lei

TITLE OF INVENTION: Mu Opioid Receptors: Compositions and Methods

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P. O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/889,108

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/305,518

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Wilson, Mark B.

REGISTRATION NUMBER: 37,259

REFERENCE/DOCKET NUMBER: INDA005\WIM

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512-418-3000

TELEFAX: 512-474-7577

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1618 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (cDNA)

FEATURE:

NAME/KEY: CDS

LOCATION: 339..1235

US-08-889-108-3

Query Match 38.5%; Score 444.8; DB 3; Length 1618;

Best Local Similarity 66.8%; Pred. No. 4.9e-104;

Matches 667; Conservative 0; Mismatches 322; Indels 9; Gaps 2;

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Db 350 ACCGACCGGGCTTGGCGGGAACGACAGCGCTGTGCGCTCAGACCGCGAGCCCTTCCATGG 409

QY 170 CCATCCCGGTCAATCATCAGCGGGTCTACTCCGCTAGTGTTCGTCGGGGCTTGGTGGCA 229

Db 410 TCACAGCCATTACCATATGGCCCTCTACTCTATCGTGTGTAGTGGGCTCTTCGGAA 469

QY 230 ACTCGCTGGTCAATGTTTCGTGATCATCCGATACACAAAGATGAAGACGACCAACCAATTT 289

Db 470 ACTTCTGGTCAATGATGTGATTGAAGATACACCAAAATGAAGACTGCCACCAACATCT 529

QY 290 ACATATTAACTGGCTTTGGCAGATGCTTTAGTTACTACCAACATGCCCTTTTCAGAGTA 349

Db 530 ACATTTTCAACCTTGCTCTGGCAGACGCTTAGCGACCACTACACTGCCCTTTTCAGAGT 589

QY 350 CGGTCTACTTGATGAATTTCTCGCCCTTTTGGGGATGTGTGTGCAAGATAGTAATTTCCA 409

Db 590 TCAACTACCTGATGGAAACATGSCCTTCGGAACCATCTCTGCAAGATCGTATCTCAA 649

QY 410 TTGATTACTACAAATGTTTCAACAGATCTTCACTTGACCATGATGAGCGTGGACCGCT 469



GenCore version 5.1.6  
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Perfect score: 1154  
Sequence: 1 atggactcccgatccagat.....ccagatgactagctgtgga 1154

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 11230502

Minimum DB seq length: 0

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Maximum Match 100%  
Listing first 45 summaries

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22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1152.4	99.9	1602	19	US-10-278-598-559
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8	1150.8	99.7	1154	11	US-09-904-584-6
9	1150.8	99.7	1154	11	US-09-904-584-7
10	1144.4	99.2	1182	15	US-10-225-567A-147
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12	1144.4	99.2	1182	17	US-10-305-720-1417
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14	1141.4	98.9	1143	16	US-10-318-661-1
15	1136.2	98.5	1284	15	US-10-318-661-3
16	1133.4	98.2	1143	15	US-10-345-880-21
17	1130.2	97.9	1143	10	US-09-826-509-542
18	1130.2	97.9	1143	19	US-10-925-095-542
19	999.4	86.6	1275	16	US-10-318-661-5
20	994.6	86.2	1275	16	US-10-318-661-7
21	979.4	84.9	1875	16	US-10-318-661-13
22	963.4	83.5	1875	16	US-10-318-661-15
23	909.2	78.8	1408	9	US-09-214-904-5
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30	444.8	38.5	1618	10	US-09-841-720-3
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ALIGNMENTS

RESULT 1

US-09-904-584-4  
; Sequence 4, Application US/09904584  
; Publication No. US20040097704A1  
; GENERAL INFORMATION:  
; APPLICANT: Kreek, Mary Jeanne  
; APPLICANT: Yufarov, Vadim  
; APPLICANT: LaForge, Karl Steven  
; TITLE OF INVENTION: Alleles of the Human Kappa Opioid  
; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods  
; TITLE OF INVENTION: Methods of Treatment Based Thereon  
; FILE REFERENCE: 600-1-285N  
; CURRENT APPLICATION NUMBER: US/09/904,584  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: 60/218,300  
; PRIOR FILING DATE: 2000-07-14  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 1154  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-09-904-584-4

Query Match 100.0%; Score 1154; DB 11; Length 1154;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 ATGGACTCCCGATCCAGATCTTCGGGGGAGCGGGCCCTACCTGGCCCCGAGCGCC 60  
Qy 61 TGCTGCCCCCAACAGCAGCGCTGTGTTCCCGGTGGCGCGAGCCCGACGACGAGCGGC 120

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Qy      301  CTGGCTTTGGCAGATGCTTTAGTTACTACAAACATGCCCTTTTCCAGTAGTGGTCTT 360
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Qy      781  GGCTCCCGAGAGAAGATCGCAACCTCGTAGGATCAACAGACTGGTCTGGTGGTG 840
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Qy      841  GCAGTCTTGGTCTGCTGAGATCCCAATTCACATATTCATCTGAGGAGGCTCTGGG 900
Db      841  GCAGTCTTGGTCTGCTGAGATCCCAATTCACATATTCATCTGAGGAGGCTCTGGG 900
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Qy      1021  TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGACAGCACTAGCAGATC 1080
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Qy      1081  CGAATACAGTTTCCAGTCTGCTTCTGAGGAGCAATCGATGGGATGAATTAACAGTA 1140
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RESULT 2

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US-09-904-584-1
; Sequence 1, Application US/09904584
; Publication No. US2004009704A1
; GENERAL INFORMATION:
; APPLICANT: Kreek, Mary Jeanne
; APPLICANT: Yufarov, Vadim
; APPLICANT: Laforge, Karl Steven
; TITLE OF INVENTION: Alleles of the Human Kappa Opioid
; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods Using Said Alleles, and
; TITLE OF INVENTION: Methods of Treatment Based Thereon
; FILE REFERENCE: 600-1-285N
; CURRENT APPLICATION NUMBER: US/09/904,584
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/218,300
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-904-584-1

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Query Match          99.9%; Score 1152.4; DB 11; Length 1154;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1153; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  ATGGACTCCCCGATCCAGATCTTCCGCGGAGCGCGGCTTCTGCTGGCGCCCTTCTGCGCCCGGAGCGCC 60
Db      1  ATGGACTCCCCGATCCAGATCTTCCGCGGAGCGCGGCTTCTGCTGGCGCCCTTCTGCGCCCGGAGCGCC 60
Qy      61  TGCTTCCGCCCCCAACAGCAGCGCTTCTCCGCTGGCGGAGCGCGGAGCGCGCAACCGC 120
Db      61  TGCTTCCGCCCCCAACAGCAGCGCTTCTCCGCTGGCGGAGCGCGGAGCGCGCAACCGC 120
Qy      121  AGCGCGGCTCGGAGGAGCGCGAGCTGGAGCGCGGCAATCTCCCGGCGCATCTCCCGGCGATCCCGGTC 180
Db      121  AGCGCGGCTCGGAGGAGCGCGAGCTGGAGCGCGGCAATCTCCCGGCGCATCTCCCGGCGATCCCGGTC 180
Qy      181  ATCATCAGCGGCTCTACTCCGTAGTGTTCGTGGGCTGGTGGCAACTCGCTGGTC 240
Db      181  ATCATCAGCGGCTCTACTCCGTAGTGTTCGTGGGCTGGTGGCAACTCGCTGGTC 240
Qy      241  ATGTTCTGATCATCCGATACCAAGATGAAGACAGCAACCAATTTTACATATTTAC 300
Db      241  ATGTTCTGATCATCCGATACCAAGATGAAGACAGCAACCAATTTTACATATTTAC 300
Qy      301  CTGGCTTTGGCAGATGCTTTAGTTACTACAAACATGCCCTTTTCCAGTAGTGGTCTT 360
Db      301  CTGGCTTTGGCAGATGCTTTAGTTACTACAAACATGCCCTTTTCCAGTAGTGGTCTT 360
Qy      361  ATGAATTCCTGGCTTTGGGATGCTCTGCAAGATAGTAAATTTCCATTTGATTACT 420
Db      361  ATGAATTCCTGGCTTTGGGATGCTCTGCAAGATAGTAAATTTCCATTTGATTACT 420
Qy      421  AACATGTTTCCAGCATCTTCCATCTTGAACCATGATGAGCGTGGACCGTACATATC 480
Db      421  AACATGTTTCCAGCATCTTCCATCTTGAACCATGATGAGCGTGGACCGTACATATC 480
Qy      481  TGCCACCCCGTGAAGCTTTGGACTTTCCGACACCCCTTGAAGCAAGATCATATATC 540
Db      481  TGCCACCCCGTGAAGCTTTGGACTTTCCGACACCCCTTGAAGCAAGATCATATATC 540
Qy      541  TGCCATCTGGCTGCTGCTCATCTGTTGGATCTCTGCAATAGTCTTGGAGGACCAAA 600
Db      541  TGCCATCTGGCTGCTGCTCATCTGTTGGATCTCTGCAATAGTCTTGGAGGACCAAA 600
Qy      601  GTACAGGAAGACGTCGATGTCATTGAGTGTCTTCCAGTTCCTGAGATGATGATCTCC 660
Db      601  GTACAGGAAGACGTCGATGTCATTGAGTGTCTTCCAGTTCCTGAGATGATGATCTCC 660

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Qy	661	TGTTGGGACCTCTTTCATGAAGATCTGGCTCTTCATCTTTGGCTTCGTGATCCCTGTCCTC	720
Db	661		
Qy	721	ATCATCATCGTCTGGTACACCTGATGATCCTGGGTCTCAAGAGCGTCCGGCTCCTTTCT	780
Db	721		
Qy	781	GGCTCCCGAGAGAAAGATCGCAACTCGTGGTAGGATCACGACATGGCTCTCGTGGTGGTG	840
Db	781		
Qy	841	GCAGTCTTTGTCGTCTGCTGGACTCCCATTCACATATTCATCTCGTGGAGGCTCTGGGG	900
Db	841		
Qy	901	AGCACCTCCCAACAGACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT	960
Db	901		
Qy	961	ACCAACAGTAGCCTGAATCCCATTTCTACGCCCTTTCTTGATGAAAATTTCAAGCGGTGT	1020
Db	961		
Qy	1021	TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGATGGAGCGGACAGACCTAGCAGAGTC	1080
Db	1021		
Qy	1081	CGAAATACAGTTCAGGATCCTTGCTTACCTGAGGGACATCGATGGGATGAATAAACCACTA	1140
Db	1081		
Qy	1141	TGACTAGTCGTGGA	1154
Db	1141		

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RESULT 3
US-10-278-698-45
; Sequence 45, Application US/10278698
; Publication No. US20050037344A1
; GENERAL INFORMATION:
; APPLICANT: PathoArray GmbH
; APPLICANT: Stuhlmüller, Bruno
; APPLICANT: Haupl, Thomas
; TITLE OF INVENTION: Nucleic Acid Array
; FILE REFERENCE: O30027US
; CURRENT APPLICATION NUMBER: US/10/278,698
; CURRENT FILING DATE: 2002-10-23
; NUMBER OF SEQ ID NOS: 1050
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
; LENGTH: 1602
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-278-698-45

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	Query Match	99.9%	Score 1152.4	DB 19	Length 1602
	Best Local Similarity	99.9%	Pred. No. 0		
	Matches 1153	Conservative 0	Mismatches 1	Indels 0	Gaps 0
Qy	1	ATGACATCCCCGATCCAGATCTTCCGGGGAGCGGGCCCTACTCTGGCCCCGAGCGCC	60		
Db	376	ATGACATCCCCGATCCAGATCTTCCGGGGAGCGGGCCCTACTCTGGCCCCGAGCGCC	435		
Qy	61	TGCCTGCCCCCCCAACAGCAGCGCCCTGTGTTTCCCGGCTGGGCGGAGCCCGACAGCAACGGC	120		
Db	436	TGCCTGCCCCCCCAACAGCAGCGCCCTGTGTTTCCCGGCTGGGCGGAGCCCGACAGCAACGGC	495		
Qy	121	AGCGCGGGCTCGAGGACGCGCAGCTGGAGCGCCCGGCACATCTCTCCCGGGCATCCCGGT	180		
Db	496	AGCGCGGGCTCGAGGACGCGCAGCTGGAGCGCCCGGCACATCTCTCCCGGGCATCCCGGT	555		

QY	181	ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGCGTGGGCTTGGTGGGCAACTCCGTGGTC	240
Db	556	ATCATCACGGCGGTCTACTCCGTAGTGTTCGTGCGTGGGCTTGGTGGGCAACTCCGTGGTC	615
QY	241	ATGTTTCGTGATCATCCGATACACAAGATGAAGACAGCAACCAACATTTACATATTTAAC	300
Db	616	ATGTTTCGTGATCATCCGATACACAAGATGAAGACAGCAACCAACATTTACATATTTAAC	675
QY	301	CTGGCTTTGGCAGATGCTTTTAGTTACTTACAACCATGCCCCTTTCAGAGTAGCGGTCTACTTG	360
Db	676	CTGGCTTTGGCAGATGCTTTTAGTTACTTACAACCATGCCCCTTTCAGAGTAGCGGTCTACTTG	735
QY	361	ATGAATTCCTGGCCCTTTTGGGGATGTCTGTGCAAGATAGTAATTTCCATTGATTACTAC	420
Db	736	ATGAATTCCTGGCCCTTTTGGGGATGTCTGTGCAAGATAGTAATTTCCATTGATTACTAC	795
QY	421	AACATGTTCCACAGCATCTTCACTTGACCATGATGAGCGTGACCGCTACATTGCGGTG	480
Db	796	AACATGTTCCACAGCATCTTCACTTGACCATGATGAGCGTGACCGCTACATTGCGGTG	855
QY	481	TGCCACCCCGTGAAGGCTTTTGGACTTCGCGCACACCCCTTGAAGGCAAAAGATCATCAATATC	540
Db	856	TGCCACCCCGTGAAGGCTTTTGGACTTCGCGCACACCCCTTGAAGGCAAAAGATCATCAATATC	915
QY	541	TGCATCTGGCTGTCTGTCGTATCTCTGTTTGGCATCTCTGCAATAGTCTCTTGGAGGACCAAA	600
Db	916	TGCATCTGGCTGTCTGTCGTATCTCTGTTTGGCATCTCTGCAATAGTCTCTTGGAGGACCAAA	975
QY	601	GTCAGGGAAGACGTCGATGTCATTGAGTGCTCTTCGAGTTCCTCCAGATGATGACTACTCC	660
Db	976	GTCAGGGAAGACGTCGATGTCATTGAGTGCTCTTCGAGTTCCTCCAGATGATGACTACTCC	1035
QY	661	TGTTGGGACCTTTTCATGAAGATCTGCGTCTTCATCTTTGSCCTTCGTGATCCCTGTCCCTC	720
Db	1036	TGTTGGGACCTTTTCATGAAGATCTGCGTCTTCATCTTTGSCCTTCGTGATCCCTGTCCCTC	1095
QY	721	ATCATCATGCTGTCTACACCTGTGATGATCCTGCGTCTCAAGACGTCGCGCTCCTTTCT	780
Db	1096	ATCATCATGCTGTCTACACCTGTGATGATCCTGCGTCTCAAGACGTCGCGCTCCTTTCT	1155
QY	781	GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACAGACTGGTCTCTGGTGGTGGTG	840
Db	1156	GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACAGACTGGTCTCTGGTGGTGGTG	1215
QY	841	GCAGTCTTCGTGCTGTCTGGACTCCCATTCACATATTCATCTCTGTGGAGGCTCTGGGG	900
Db	1216	GCAGTCTTCGTGCTGTCTGGACTCCCATTCACATATTCATCTCTGTGGAGGCTCTGGGG	1275
QY	901	AGCACCTCCACAGCAGCAGTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT	960
Db	1276	AGCACCTCCACAGCAGCAGTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT	1335
QY	961	ACCAACAGTAGCCTGAAATCCCATTTCTACGCGCTTTCTTGATGAAAATTTCAAGCGGTGT	1020
Db	1336	ACCAACAGTAGCCTGAAATCCCATTTCTACGCGCTTTCTTGATGAAAATTTCAAGCGGTGT	1395
QY	1021	TTCGGGACTTCTGCTTTTCCACTGGAAGATGAGGATGGAGCGGACAGCAGCTACGAGTC	1080
Db	1396	TTCGGGACTTCTGCTTTTCCACTGGAAGATGAGGATGGAGCGGACAGCAGCTACGAGTC	1455
QY	1081	CGAATACAGTTCAGGATCCTGCTTACCTGAGGACATCGATCGGATGAATAACAGTA	1140
Db	1456	CGAATACAGTTCAGGATCCTGCTTACCTGAGGACATCGATCGGATGAATAACAGTA	1515
QY	1141	TGACTAGTCGTGGA	1154
Db	1516	TGACTAGTCGTGGA	1529

RESULT 4

US-10-278-698-559

i Sequence 559, Application US/10278698

RESULT 4  
US-10-278-698-559  
; Sequence 559, Application US/10278698

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; Publication No. US20050037344A1
; GENERAL INFORMATION:
; APPLICANT: Pathoarray GmbH
; APPLICANT: Stuhlmüller, Bruno
; APPLICANT: Haupt, Thomas
; TITLE OF INVENTION: Nucleic Acid Array
; FILE REFERENCE: 030027US
; CURRENT APPLICATION NUMBER: US/10/278,698
; CURRENT FILING DATE: 2002-10-23
; NUMBER OF SEQ ID NOS: 1050
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 559
; LENGTH: 1602
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-278-698-559

Query Match          99.9%; Score 1152.4; DB 19; Length 1602;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1153; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGCCCTACCTGGCGCCCGGAGCGGC 60
DB      376  ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGCCCTACCTGGCGCCCGGAGCGGC 435

QY      61  TGCCTGCCCGCCCAACAGACGCGCTGTGTTCCCGGCTGGGCGAGCCCGACAGCAACGCG 120
DB      436  TGCCTGCCCGCCCAACAGACGCGCTGTGTTCCCGGCTGGGCGAGCCCGACAGCAACGCG 495

QY      121  AGCGCGGCTCGGAGGACGCGAGCTGGAGCGCGGACATCTCCCGCGCCATCCCGGTC 180
DB      496  AGCGCGGCTCGGAGGACGCGAGCTGGAGCGCGGACATCTCCCGCGCCATCCCGGTC 555

QY      181  ATCATCAGCGCGTCTACTCCGTAGTGTGCTGCGGGCTTGTGGGCAACTCGCTGGTC 240
DB      556  ATCATCAGCGCGTCTACTCCGTAGTGTGCTGCGGGCTTGTGGGCAACTCGCTGGTC 615

QY      241  ATGTTCTGTATATCCGATACACAAAGATGAAGACAGCAACCAATTTACATATTAAAC 300
DB      616  ATGTTCTGTATATCCGATACACAAAGATGAAGACAGCAACCAATTTACATATTAAAC 675

QY      301  CTGGCTTTGGCAGATGCTTTAGTTACTACAAACATCCCTTTTCAGAGTACGGTCTACTTG 360
DB      676  CTGGCTTTGGCAGATGCTTTAGTTACTACAAACATCCCTTTTCAGAGTACGGTCTACTTG 735

QY      361  ATCAATTCCTGGGCTTTGGGATGTGCTGTGAAGATAGTAATTTCCATTGATTAATAC 420
DB      736  ATCAATTCCTGGGCTTTGGGATGTGCTGTGAAGATAGTAATTTCCATTGATTAATAC 480

QY      421  AACATGTTACACGATCTTTCACCTTGACCATGATGAGCGTGACCGCTACATTGCGGTG 480
DB      796  AACATGTTACACGATCTTTCACCTTGACCATGATGAGCGTGACCGCTACATTGCGGTG 855

QY      481  TGCCACCCCGTGAAGGCTTTGGACTTCCGACACCCCTTGAAGCAAGATATCAATATC 540
DB      856  TGCCACCCCGTGAAGGCTTTGGACTTCCGACACCCCTTGAAGCAAGATATCAATATC 915

QY      541  TGCACTGGCTGTGCTGCTCATCTGTGGATCTCTGCAATAGTCTCTTGGAGGACCAAA 600
DB      916  TGCACTGGCTGTGCTGCTCATCTGTGGATCTCTGCAATAGTCTCTTGGAGGACCAAA 975

QY      601  GTCAGGGAAGACGCTCGATGTCATTGATGCTCTTGCAGTTCCAGATGATGATGATCTCC 660
DB      976  GTCAGGGAAGACGCTCGATGTCATTGATGCTCTTGCAGTTCCAGATGATGATGATCTCC 1035

QY      661  TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCGCTTCGATCCCTGTCCTC 720
DB      1036  TGGTGGGACCTCTTCATGAAGATCTGCGTCTTCATCTTTGCGCTTCGATCCCTGTCCTC 1095

QY      721  ATCATCATCGTCTGCTACACCCCTGATGATCCTCGGCTCTCAAGAGCGTCCGGCTCTTCT 780
DB      1096  ATCATCATCGTCTGCTACACCCCTGATGATCCTCGGCTCTCAAGAGCGTCCGGCTCTTCT 1155

; Publication No. US09904584-2
; Sequence 2, Application US/09904584
; Publication No. US20040097704A1
; GENERAL INFORMATION:
; APPLICANT: Kreek, Mary Jeanne
; APPLICANT: Yuferov, Vadim
; APPLICANT: LaForge, Karl Steven
; TITLE OF INVENTION: Alleles of the Human Kappa Opioid
; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods Using Said Alleles, and
; TITLE OF INVENTION: Methods of Treatment Based Thereon
; FILE REFERENCE: 600-1-285N
; CURRENT APPLICATION NUMBER: US/09/904,584
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/218,300
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-904-584-2

QY      781  GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACACAGACTGCTCTGGTGGTGGTG 840
DB      1156  GGCTCCCGAGAGAAAGATCGCAACCTGCGTAGGATCACACAGACTGCTCTGGTGGTGGTG 1215

QY      841  GCAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
DB      1216  GCAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1275

QY      901  AGCACCTCCACAGACAGACGCTGCTCTCTCCAGCTATTCTCTGCAATCGCCTTAGGCTAT 960
DB      1276  AGCACCTCCACAGACAGACGCTGCTCTCTCCAGCTATTCTCTGCAATCGCCTTAGGCTAT 1335

QY      961  ACCAACAGTAGCTGAATCCCATTTCTACGGCTTTCTTGTAGTAAATTTCAAGCGGTGT 1020
DB      1336  ACCAACAGTAGCTGAATCCCATTTCTACGGCTTTCTTGTAGTAAATTTCAAGCGGTGT 1395

QY      1021  TTCCGGGACTTCTGCTTTTCCACTGAAGATGAGATGAGGAGCGGAGAGCTAGCAGAGTC 1080
DB      1396  TTCCGGGACTTCTGCTTTTCCACTGAAGATGAGATGAGGAGCGGAGAGCTAGCAGAGTC 1455

QY      1081  CGAAATACAGTTACAGATCTCTGCTTACCTGAGGACATCGATGGGATGAATAAACAGTA 1140
DB      1456  CGAAATACAGTTACAGATCTCTGCTTACCTGAGGACATCGATGGGATGAATAAACAGTA 1515

QY      1141  TGACTAGTCTGTGA 1154
DB      1516  TGACTAGTCTGTGA 1529

RESULT 5
US-09-904-584-2
; Sequence 2, Application US/09904584
; Publication No. US20040097704A1
; GENERAL INFORMATION:
; APPLICANT: Kreek, Mary Jeanne
; APPLICANT: Yuferov, Vadim
; APPLICANT: LaForge, Karl Steven
; TITLE OF INVENTION: Alleles of the Human Kappa Opioid
; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods Using Said Alleles, and
; TITLE OF INVENTION: Methods of Treatment Based Thereon
; FILE REFERENCE: 600-1-285N
; CURRENT APPLICATION NUMBER: US/09/904,584
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/218,300
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1154
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-904-584-2

Query Match          99.7%; Score 1150.8; DB 11; Length 1154;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGCCCTACCTGGCGCCCGGAGCGGC 60
DB      1  ATGGACTCCCGATCCAGATCTTCCGCGGGGAGCCGGCCCTACCTGGCGCCCGGAGCGGC 60

QY      61  TGCCTGCCCGCCCAACAGACGCGCTGTTTCCCGGCTGGGCGGAGCCCGGAGCAACGCG 120
DB      61  TGCCTGCCCGCCCAACAGACGCGCTGTTTCCCGGCTGGGCGGAGCCCGGAGCAACGCG 120

QY      121  AGCGCGGCTCGGAGGACGCGAGCTGGAGCGCGGACATCTCCCGCGGCTCCCGGTC 180
DB      121  AGCGCGGCTCGGAGGACGCGAGCTGGAGCGCGGACATCTCCCGCGGCTCCCGGTC 180

QY      181  ATCATCAGCGGCTCTACTCCGTAGTGTTCGTCGGGCTTGGTGGGCAACTCGCTGGTC 240
DB      181  ATCATCAGCGGCTCTACTCCGTAGTGTTCGTCGGGCTTGGTGGGCAACTCGCTGGTC 240
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Qy 241 ATGTTCTGATCATCCGATACACAAAGATGAAGACAGCAACAAATTTACATATTAAAC 300
Db 241 ATGTTCTGATCATCCGATACACAAAGATGAAGACAGCAACAAATTTACATATTAAAC 300
Qy 301 CTGGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCGCTTTTCAGAGTACGGTCTACTTG 360
Db 301 CTGGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCGCTTTTCAGAGTACGGTCTACTTG 360
Qy 361 ATGAATCTCTGGCCCTTTGGGATGCTGTCAGATAGTAATTTCCATTTGATTTACTAC 420
Db 361 ATGAATCTCTGGCCCTTTGGGATGCTGTCAGATAGTAATTTCCATTTGATTTACTAC 420
Qy 421 AACATGTTCCAGAGATCTTACCTTGACCATGATGAGCGGTGACCGCTCATTTGCCGTG 480
Db 421 AACATGTTCCAGAGATCTTACCTTGACCATGATGAGCGGTGACCGCTCATTTGCCGTG 480
Qy 481 TGCCACCCCGTGAAGGCTTTCGACTTCGCGACACCCCTTGAAGGCAAGATCATCAATATC 540
Db 481 TGCCACCCCGTGAAGGCTTTCGACTTCGCGACACCCCTTGAAGGCAAGATCATCAATATC 540
Qy 541 TGCACTCTGGCTGCTGCTCATCTGTTGGCATCTCTGCAATAGTCTTTGGAGGCAACAAA 600
Db 541 TGCACTCTGGCTGCTGCTCATCTGTTGGCATCTCTGCAATAGTCTTTGGAGGCAACAAA 600
Qy 601 GTCAGGGAAGAGTCGATGTCATTTAGTGTCTCTTGCAGTTCCAGATGATGATCTCTCC 660
Db 601 GTCAGGGAAGAGTCGATGTCATTTAGTGTCTCTTGCAGTTCCAGATGATGATCTCTCC 660
Qy 661 TGGTGGGACCTTTCATGAGATCTGCGTCTTCTATCTTTGCTTTCGATCCCTGCTCTC 720
Db 661 TGGTGGGACCTTTCATGAGATCTGCGTCTTCTATCTTTGCTTTCGATCCCTGCTCTC 720
Qy 721 ATCATCATCTGCTGTCTACACCTGATGATCTGCGTCTCTCAAGAGCGTCCGCTCTTCT 780
Db 721 ATCATCATCTGCTGTCTACACCTGATGATCTGCGTCTCTCAAGAGCGTCCGCTCTTCT 780
Qy 781 GGCTCCCGAGAGAAGATCGCAACCTGCTAGGATCACAGACTGGTCTCTGGTGGTG 840
Db 781 GGCTCCCGAGAGAAGATCGCAACCTGCTAGGATCACAGACTGGTCTCTGGTGGTG 840
Qy 841 GCAGTCTCTGCTGCTGCTGACTCCCATTTACATATTATTCATCTCTGGTGGAGCTCTGGG 900
Db 841 GCAGTCTCTGCTGCTGCTGACTCCCATTTACATATTATTCATCTCTGGTGGAGCTCTGGG 900
Qy 901 AGCACTCTCCACAGACAGCTGCTCTCTCCAGCTATTACTCTGATCGCTTAGGCTAT 960
Db 901 AGCACTCTCCACAGACAGCTGCTCTCTCCAGCTATTACTCTGATCGCTTAGGCTAT 960
Qy 961 ACCAAGTACGCTGAATCCCATCTCTACGCTTTCTTGTATGAAATTTCAAGCGGTGT 1020
Db 961 ACCAAGTACGCTGAATCCCATCTCTACGCTTTCTTGTATGAAATTTCAAGCGGTGT 1020
Qy 1021 TTCCGGGACTTCTGCTTTCAGTGAAGATGAGGATGAGCGGACAGACACTAGCAGAGTC 1080
Db 1021 TTCCGGGACTTCTGCTTTCAGTGAAGATGAGGATGAGCGGACAGACACTAGCAGAGTC 1080
Qy 1081 CGAAATACAGTTTCAGGATCTGCTTACCTGAGGACATCGATGAGTGAATAAACACAGTA 1140
Db 1081 CGAAATACAGTTTCAGGATCTGCTTACCTGAGGACATCGATGAGTGAATAAACACAGTA 1140
Qy 1141 TGACTAGTCGTGA 1154
Db 1141 TGACTAGTCGTGA 1154

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RESULT 6  
 US-09-904-584-3  
 ; Sequence 3, Application US/09904584  
 ; Publication No. US20040097704A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kreek, Mary Jeanne  
 ; APPLICANT: Yuforov, Vadim  
 ; APPLICANT: LaForge, Karl Steven

; TITLE OF INVENTION: Alleles of the Human Kappa Opioid  
 ; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods Using Said Alleles, and  
 ; FILE REFERENCE: 600-1-285N  
 ; CURRENT APPLICATION NUMBER: US/09/904,584  
 ; CURRENT FILING DATE: 2001-07-13  
 ; PRIOR APPLICATION NUMBER: 60/219,300  
 ; PRIOR FILING DATE: 2000-07-14  
 ; NUMBER OF SEQ ID NOS: 7  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 3  
 ; LENGTH: 1154  
 ; TYPE: DNA  
 ; ORGANISM: homo sapiens  
 US-09-904-584-3

Query Match 99.7%; Score 1150.8; DB 11; Length 1154;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 ATGCACTCCCGATCCAGATCTTCCGCGGAGCGCGCCCTACTCGCGCCCGAGCGCC 60
Db 1 ATGCACTCCCGATCCAGATCTTCCGCGGAGCGCGCCCTACTCGCGCCCGAGCGCC 60
Qy 61 TGCCTGCCCCCAAACAGCAGCGCTGTTTCCCGCTGGCGCCGAGCCCGACAGCAACGGC 120
Db 61 TGCCTGCCCCCAAACAGCAGCGCTGTTTCCCGCTGGCGCCGAGCCCGACAGCAACGGC 120
Qy 121 AGCGCCGGCTCGAGGAGCGCAGCTGAGCGCCCGGACATCTCCCGCGCCATCCCGGTC 180
Db 121 AGCGCCGGCTCGAGGAGCGCAGCTGAGCGCCCGGACATCTCCCGCGCCATCCCGGTC 180
Qy 181 ATCATCATCGCGCTCTACTCCGTAGTGTCTGCTGCTGGCTTGGTGGCACTCGCTGTC 240
Db 181 ATCATCATCGCGCTCTACTCCGTAGTGTCTGCTGCTGGCTTGGTGGCACTCGCTGTC 240
Qy 241 ATGTTCTGATCATCCGATACACAAAGATGAAGACAGCAACAAATTTACATATTAAAC 300
Db 241 ATGTTCTGATCATCCGATACACAAAGATGAAGACAGCAACAAATTTACATATTAAAC 300
Qy 301 CTGGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCGCTTTTCAGAGTACGGTCTACTTG 360
Db 301 CTGGCTTTGGCAGATGCTTTAGTTACTACAAACCATGCGCTTTTCAGAGTACGGTCTACTTG 360
Qy 361 ATGAATCTCTGGCCCTTTGGGATGCTGTCAGATAGTAATTTCCATTTGATTTACTAC 420
Db 361 ATGAATCTCTGGCCCTTTGGGATGCTGTCAGATAGTAATTTCCATTTGATTTACTAC 420
Qy 421 AACATGTTCCAGAGATCTTACCTTGACCATGATGAGCGGTGACCGCTCATTTGCCGTG 480
Db 421 AACATGTTCCAGAGATCTTACCTTGACCATGATGAGCGGTGACCGCTCATTTGCCGTG 480
Qy 481 TGCCACCCCGTGAAGGCTTTCGACTTCGCGACACCCCTTGAAGGCAAGATCATCAATATC 540
Db 481 TGCCACCCCGTGAAGGCTTTCGACTTCGCGACACCCCTTGAAGGCAAGATCATCAATATC 540
Qy 541 TGCACTCTGGCTGCTGCTCATCTGTTGGCATCTCTGCAATAGTCTTTGGAGGCAACAAA 600
Db 541 TGCACTCTGGCTGCTGCTCATCTGTTGGCATCTCTGCAATAGTCTTTGGAGGCAACAAA 600
Qy 601 GTCAGGGAAGAGTCGATGTCATTTAGTGTCTCTTGCAGTTCCAGATGATGATCTCTCC 660
Db 601 GTCAGGGAAGAGTCGATGTCATTTAGTGTCTCTTGCAGTTCCAGATGATGATCTCTCC 660
Qy 661 TGGTGGGACCTTTCATGAGATCTGCGTCTTCTATCTTTGCTTTCGATCCCTGCTCTC 720
Db 661 TGGTGGGACCTTTCATGAGATCTGCGTCTTCTATCTTTGCTTTCGATCCCTGCTCTC 720
Qy 721 ATCATCATCTGCTGTCTACACCTGATGATCTGCGTCTCTCAAGAGCGTCCGCTCTTCT 780
Db 721 ATCATCATCTGCTGTCTACACCTGATGATCTGCGTCTCTCAAGAGCGTCCGCTCTTCT 780
Qy 781 GGCTCCCGAGAGAAGATCGCAACCTGCTAGGATCACAGACTGGTCTCTGGTGGTG 840

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;; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods Using Said Alleles, and  
;; TITLE OF INVENTION: Methods of Treatment Based Thereon  
;; FILE REFERENCE: 600-1-285N  
;; CURRENT APPLICATION NUMBER: US/09/904,584  
;; PRIOR FILING DATE: 2001-07-13  
;; PRIOR APPLICATION NUMBER: 60/218,300  
;; PRIOR FILING DATE: 2000-07-14  
;; NUMBER OF SEQ ID NOS: 7  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 6  
;; LENGTH: 1154  
;; TYPE: DNA  
;; ORGANISM: homo sapiens  
US-09-904-584-6

Query Match 99.7%; Score 1150.8; DB 11; Length 1154;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGACTCCCCCGATCCAGATCTTCGCGGGGAGCGGCCCTTACCTGCGCCCCGAGCGCC 60  
Db 1 ATGACTCCCCCGATCCAGATCTTCGCGGGGAGCGGCCCTTACCTGCGCCCCGAGCGCC 60

Qy 61 TGCCTGCCCCCAACAGCAGCGCCCTGTTTCCGGCTGGGCGGAGCCGCAAGCAAGCGC 120  
Db 61 TGCCTGCCCCCAACAGCAGCGCCCTGTTTCCGGCTGGGCGGAGCCGCGCAAGCAAGCGC 120

Qy 121 AGCGCGGCTCGGAGGAGCGCAGCTGGAGCGCCGCGCACATCTCCCGCCCATCCCGGTC 180  
Db 121 AGCGCGGCTCGGAGGAGCGCAGCTGGAGCGCCGCGCACATCTCCCGCCCATCCCGGTC 180

Qy 181 ATCATCAGCGGCTACTCCGTAAGTGTTCGTCGGGCTTGGTGGGCAACTCGCTGTC 240  
Db 181 ATCATCAGCGGCTACTCCGTAAGTGTTCGTCGGGCTTGGTGGGCAACTCGCTGTC 240

Qy 241 ATGTTCTGTATCCCGATACAAAGATGAAGACAGCAACCAATTTACATATTAAAC 300  
Db 241 ATGTTCTGTATCCCGATACAAAGATGAAGACAGCAACCAATTTACATATTAAAC 300

Qy 301 CTGCTTTGGCAGATGCTTTAGTTACTACACCATGCGCTTTCAGGTACGGTCTACTTG 360  
Db 301 CTGCTTTGGCAGATGCTTTAGTTACTACACCATGCGCTTTCAGGTACGGTCTACTTG 360

Qy 361 ATGAATTCCTGGCTTTGGGAGTGTCTGTCGAAGATAGTAATTTCCATTGATTACTAC 420  
Db 361 ATGAATTCCTGGCTTTGGGAGTGTCTGTCGAAGATAGTAATTTCCATTGATTACTAC 420

Qy 421 AACATGTTCCAGCATCTTCACTTACCATGATGAGCGTGGACCGCTACATTTGCCGTG 480  
Db 421 AACATGTTCCAGCATCTTCACTTACCATGATGAGCGTGGACCGCTACATTTGCCGTG 480

Qy 481 TGCCACCCCGTGAAGGCTTTGGACTTCGCGACACCCCTTGAGGCAAGATCATCAATATC 540  
Db 481 TGCCACCCCGTGAAGGCTTTGGACTTCGCGACACCCCTTGAGGCAAGATCATCAATATC 540

Qy 541 TGCACTCTGGCTGCTGCTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGACCAAA 600  
Db 541 TGCACTCTGGCTGCTGCTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGACCAAA 600

Qy 601 GTCAGGGAAGACGTGCGATGTCATTGAGTGTCTTTCAGATTTCCAGATGATGACTTCC 660  
Db 601 GTCAGGGAAGACGTGCGATGTCATTGAGTGTCTTTCAGATTTCCAGATGATGACTTCC 660

Qy 661 TGGTGGGACCTTTTCATGAAGATCTGGGCTTTCATCTTTGGCTTCGTGATCCCTGTCTC 720  
Db 661 TGGTGGGACCTTTTCATGAAGATCTGGGCTTTCATCTTTGGCTTCGTGATCCCTGTCTC 720

Qy 721 ATCATCATCTGCTGCTACACCTGATGATCTGCTGCTCTCAAGAGCGTCCGCTCTTCT 780  
Db 721 ATCATCATCTGCTGCTACACCTGATGATCTGCTGCTCTCAAGAGCGTCCGCTCTTCT 780

Qy 781 GGCTCCCGAGAGAAGATCGCAACCTCGGTAGGATCACAGACTGGTCTGCTGGTGGTG 840  
Db 781 GGCTCCCGAGAGAAGATCGCAACCTCGGTAGGATCACAGACTGGTCTGCTGGTGGTG 840

Db 781 GGCTCCCGAGAGAAGATCGCAACCTCGGTAGGATCACAGACTGGTCTGCTGGTGGTG 840  
Qy 841 GCAGTCTTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
Db 841 GCGGTCTTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
Qy 901 AGCACCTTCCACAGCAGCAGCTGCTCTCTCCAGCTATTACTTCTGTCATCGCTTAGGCTAT 960  
Db 901 AGCACCTTCCACAGCAGCAGCTGCTCTCTCCAGCTATTACTTCTGTCATCGCTTAGGCTAT 960  
Qy 961 ACCAAGAGTAGCTGAATCCCATTTCTACGCCCTTCTTGATGAAAAATTTCAAGCGGTGT 1020  
Db 961 ACCAAGAGTAGCTGAATCCCATTTCTACGCCCTTCTTGATGAAAAATTTCAAGCGGTGT 1020  
Qy 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGCGGAGAGCAGCAGTAGCAGAGTC 1080  
Db 1021 TTCCGGGACTTCTGCTTTCCACTGAAGATGAGGCGGAGAGCAGCAGTAGCAGAGTC 1080  
Qy 1081 CGAAATACAGTTACAGGATCTGCTTACTCTGAGGACATCGATGGGATGAATAAACCACTA 1140  
Db 1081 CGAAATACAGTTACAGGATCTGCTTACTCTGAGGACATCGATGGGATGAATAAACCACTA 1140  
Qy 1141 TGACTAGTCTGGA 1154  
Db 1141 TGACTAGTCTGGA 1154

RESULT 9  
US-09-904-584-7  
; Sequence 7, Application US/09904584  
; Publication No. US20040097704A1  
; GENERAL INFORMATION:  
; APPLICANT: Kreek, Mary Jeanne  
; APPLICANT: Yuforov, Vadim  
; APPLICANT: Laforge, Karl Steven  
; TITLE OF INVENTION: Alleles of the Human Kappa Opioid  
; TITLE OF INVENTION: Receptor Gene, Diagnostic Methods Using Said Alleles, and  
; TITLE OF INVENTION: Methods of Treatment Based Thereon  
; FILE REFERENCE: 600-1-285N  
; CURRENT APPLICATION NUMBER: US/09/904,584  
; CURRENT FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: 60/218,300  
; PRIOR FILING DATE: 2000-07-14  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 1154  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-09-904-584-7

Query Match 99.7%; Score 1150.8; DB 11; Length 1154;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGACTCCCCCGATCCAGATCTTCGCGGGGAGCGGCCCTTACCTGCGCCCCGAGCGCC 60  
Db 1 ATGACTCCCCCGATCCAGATCTTCGCGGGGAGCGGCCCTTACCTGCGCCCCGAGCGCC 60

Qy 61 TGCCTGCCCCCAACAGCAGCGCCCTGTTTCCGGCTGGGCGGAGCCGCAAGCAAGCGC 120  
Db 61 TGCCTGCCCCCAACAGCAGCGCCCTGTTTCCGGCTGGGCGGAGCCGCGCAAGCAAGCGC 120

Qy 121 AGCGCGGCTCGGAGGAGCGCAGCTGGAGCGCCGCGCACATCTCCCGCCCATCCCGGTC 180  
Db 121 AGCGCGGCTCGGAGGAGCGCAGCTGGAGCGCCGCGCACATCTCCCGCCCATCCCGGTC 180

Qy 181 ATCATCAGCGGCTACTCCGTAAGTGTTCGTCGGGCTTGGTGGGCAACTCGCTGTC 240  
Db 181 ATCATCAGCGGCTACTCCGTAAGTGTTCGTCGGGCTTGGTGGGCAACTCGCTGTC 240

Qy 241 ATGTTCTGTATCCCGATACAAAGATGAAGACAGCAACCAATTTACATATTAAAC 300  
Db 241 ATGTTCTGTATCCCGATACAAAGATGAAGACAGCAACCAATTTACATATTAAAC 300

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Db 241 ATGTTCTGTGATCATCGGATACAAAGATGAGACAGACCAACCAATTTACATATTTAAAC 300
Qy 301 CTGGCTTTGGCAGATGCTTTAGTTACTACAAAGATGAGTCTTTCAGAGTACGCTTACTTG 360
Db 301 CTGGCTTTGGCAGATGCTTTAGTTACTACAAAGATGAGTCTTTCAGAGTACGCTTACTTG 360
Qy 361 ATGAATTTCTGGCTTTGGGATGCTGTCAGATGATGATTTTCCATTTGATTTACTAC 420
Db 361 ATGAATTTCTGGCTTTGGGATGCTGTCAGATGATGATTTTCCATTTGATTTACTAC 420
Qy 421 AACATGTTCCACAGATCTTTACCTTTGACCATGATGAGCGTGGACCGCTACATTTGCCG 480
Db 421 AACATGTTCCACAGATCTTTACCTTTGACCATGATGAGCGTGGACCGCTACATTTGCCG 480
Qy 481 TGGCACCCTGGTGAAGCTTTGGATTTCCGACACACCTTTGAAGGCAAGATCATCAATATC 540
Db 481 TGGCACCCTGGTGAAGCTTTGGATTTCCGACACACCTTTGAAGGCAAGATCATCAATATC 540
Qy 541 TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGCACAAA 600
Db 541 TGCATCTGGCTGCTGTCGTCATCTGTTGGCATCTCTGCAATAGTCTTGGAGGCACAAA 600
Qy 601 GTGAGGAAAGATCGATGCTATGATGCTCTTCCAGTTCCTGAGTCCAGATGATGATCTCC 660
Db 601 GTGAGGAAAGATCGATGCTATGATGCTCTTCCAGTTCCTGAGTTCCTGAGTCCAGTCTCC 660
Qy 661 TGGTGGAGCTCTTTCATGAAGATCTGCTGCTTTCATCTTTGCTTCCCTGATCCCTGCTC 720
Db 661 TGGTGGAGCTCTTTCATGAAGATCTGCTGCTTTCATCTTTGCTTCCCTGATCCCTGCTC 720
Qy 721 ATCATCATCTGCTGCTACACCTCGATGATCTTGGCTCTCAAGAGCTCGCGGTCTTCT 780
Db 721 ATCATCATCTGCTGCTACACCTCGATGATCTTGGCTCTCAAGAGCTCGCGGTCTTCT 780
Qy 781 GGCTCCGAGAGAAAGATCGCACTCGTGGATCAGAGTCCAGAGTCTGCTGCTGCTGCTG 840
Db 781 GGCTCCGAGAGAAAGATCGCACTCGTGGATCAGAGTCCAGAGTCTGCTGCTGCTGCTG 840
Qy 841 GCAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Db 841 GCAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Qy 901 AGCAGCTCCACAGACAGCTGCTCTCTCCAGTATTTACTTCTGATCGCTTTAGGCTAT 960
Db 901 AGCAGCTCCACAGACAGCTGCTCTCTCCAGTATTTACTTCTGATCGCTTTAGGCTAT 960
Qy 961 ACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
Db 961 ACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
Qy 1021 TTCCGGGACTTCTGCTTCCACTGAGATGAGGATGAGGATGAGGATGAGGATGAGGATG 1080
Db 1021 TTCCGGGACTTCTGCTTCCACTGAGATGAGGATGAGGATGAGGATGAGGATGAGGATG 1080
Qy 1081 CGAAATACAGTTTCCAGTCTGCTTACCTGAGGAGATCGATGGGATGAATTAACAGTA 1140
Db 1081 CGAAATACAGTTTCCAGTCTGCTTACCTGAGGAGATCGATGGGATGAATTAACAGTA 1140
Qy 1141 TGACTAGTCTGGA 1154
Db 1141 TGACTAGTCTGGA 1154

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RESULT 10  
US-10-225-567A-147  
; Sequence 147, Application US/10225567A  
; Publication No. US20030113798A1  
; GENERAL INFORMATION:  
; APPLICANT: LifeSpan Biosciences  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burmer, Glenna C.  
; APPLICANT: Roush, Christine L.  
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS

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; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 147
; LENGTH: 1182
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-225-567A-147

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Query Match 99.2%; Score 1144.4; DB 15; Length 1182;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1148; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGGACTCCCGATCCAGATCTTCCGCGGGAGCGGCGCTTACCTGCGCCCGAGCGCC 60
Db 14 ATGGAAATCCCGATTCAGATCTTCCGCGGGAGCGCTTACCTGCGCCCGAGCGCC 73
Qy 61 TGCCTGCCCCCAACAGCAGCGCCTGCTTCCGCGCTGGCGCGAGCCCGACAGCACGCG 120
Db 74 TGCCTGCCCCCAACAGCAGCGCCTGCTTCCGCGCTGGCGCGAGCCCGACAGCACGCG 133
Qy 121 AGCGCGCGCTCGGAGAGCGCGAGCTGGAGCGCGGCACATCTCCCGCGCCATCCCGGTC 180
Db 134 AGCGCGCGCTCGGAGAGCGCGAGCTGGAGCGCGGCACATCTCCCGCGCCATCCCGGTC 193
Qy 181 ATCATCACGCGGCTTACTCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 194 ATCATCACGCGGCTTACTCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 253
Qy 241 ATGTTCTGTCATCATCCGATACCAAGATGAGACAGCAACCAACATTTACATATTTAAC 300
Db 254 ATGTTCTGTCATCATCCGATACCAAGATGAGACAGCAACCAACATTTACATATTTAAC 313
Qy 301 CTGGCTTTGGCAGATGCTTTAGTTACTACAAAGATGAGACAGCAACCAACATTTAAC 360
Db 314 CTGGCTTTGGCAGATGCTTTAGTTACTACAAAGATGAGACAGCAACCAACATTTAAC 373
Qy 361 ATGAATTTCTGGCTTTGGGATGCTGTCAGATGATGATTTTCCATTTGATTTACTAC 420
Db 374 ATGAATTTCTGGCTTTGGGATGCTGTCAGATGATGATTTTCCATTTGATTTACTAC 433
Qy 421 AACATGTTCCACAGATCTTTCACCTTGAAGATGAGCGTGGACCGCTACATTTGCCG 480
Db 434 AACATGTTCCACAGATCTTTCACCTTGAAGATGAGCGTGGACCGCTACATTTGCCG 493
Qy 481 TGCACCCCGCTGAAGCTTTGGACTTTCCGACACACCTTGAAGGCAAGATCATCAATATC 540
Db 494 TGCACCCCGCTGAAGCTTTGGACTTTCCGACACACCTTGAAGGCAAGATCATCAATATC 553
Qy 541 TGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Db 554 TGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 613
Qy 601 GTGAGGAGAGCTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db 614 GTGAGGAGAGCTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 673
Qy 661 TGGTGGGAGCTCTTTCATGAAGATCTGCTGCTTTCATCTTTGCTTCCCTGCTGCTCCT 720
Db 674 TGGTGGGAGCTCTTTCATGAAGATCTGCTGCTTTCATCTTTGCTTCCCTGCTGCTCCT 733
Qy 721 ATCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 734 ATCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 793
Qy 781 GGCTCCGAGAGAAAGATCGCACTCGTGGATCAGAGTCCAGAGTCTGCTGCTGCTGCTG 840
Db 794 GGCTCCGAGAGAAAGATCGCACTCGTGGATCAGAGTCCAGAGTCTGCTGCTGCTGCTG 853

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Qy	841	CGAGTCTTCGTGCTGCTGCAGCTCCCAATTCACATATTTCACTCTGGTGGAGGCTCTGGGG	900
Db	854	CGGGTTTTCGTCTGCTGCGACTCCCATTCACATATTTCACTCTGGTGGAGGCTCTGGGG	913
Qy	901	AGCACTCCCAACAGACAGCAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT	960
Db	914	AGCACTCCCAACAGACAGCAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTAT	973
Qy	961	ACCAACAGTAGCCTGAATCCCATCTCTTAAGCCTTTCTTGATGAAAAATTTCAAGCGGTGT	1020
Db	974	ACCAACAGTAGCCTGAATCCCATCTCTTAAGCCTTTCTTGATGAAAAATTTCAAGCGGTGT	1033
Qy	1021	TTCCGGGACTTCTGCTTTTCCACTGAAGATGAGGATGGAGCGGACAGACACTAGCAGAGTC	1080
Db	1034	TTCCGGGACTTCTGCTTTTCCACTGAAGATGAGGATGGAGCGGACAGACACTAGCAGAGTC	1093
Qy	1081	CGAAATACAGTTTCAGGATCTCGTTACCTGAGGGACATCGATGGATGAATAAAACCAAGTA	1140
Db	1094	CGAAATACAGTTTCAGGATCTCGTTACCTGAGGGACATCGATGGATGAATAAAACCAAGTA	1153
Qy	1141	TGACTAGTCGTGGA	1154
Db	1154	TGACTAGTCGTGGA	1167

RESULT 11

US-10-345-680-19

Sequence 19, Application US/10345680

Publication No. US20030148394A1

GENERAL INFORMATION:

APPLICANT: Millennium Pharmaceuticals, Inc.

APPLICANT: Silos-Santiago, Immaculada

APPLICANT: Venkateswarlu, Karicheti

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING

TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,

TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46556, 62553, 302, 323,

TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.

FILE REFERENCE: MP102-012P1RNM.OMNI

CURRENT APPLICATION NUMBER: US/10/345,680

CURRENT FILING DATE: 2003-01-16

PRIOR APPLICATION NUMBER: US 60/349,511

PRIOR FILING DATE: 2002-01-18

PRIOR APPLICATION NUMBER: US 60/360,500

PRIOR FILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: US 60/365,041

PRIOR FILING DATE: 2002-03-15

PRIOR APPLICATION NUMBER: US 60/374,063

PRIOR FILING DATE: 2002-04-19

PRIOR APPLICATION NUMBER: US 60/403,468

PRIOR FILING DATE: 2002-08-14

PRIOR APPLICATION NUMBER: US 60/414,262

PRIOR FILING DATE: 2002-09-27

PRIOR APPLICATION NUMBER: US 60/419,986

PRIOR FILING DATE: 2002-10-21

PRIOR APPLICATION NUMBER: US 60/423,809

PRIOR FILING DATE: 2002-11-05

PRIOR APPLICATION NUMBER: US 60/429,797

PRIOR FILING DATE: 2002-11-26

NUMBER OF SEQ ID NOS: 66

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 19

LENGTH: 1182

TYPE: DNA

ORGANISM: Homo Sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (14)...(1156)

US-10-345-680-19

Query Match 99.2%; Score 1144.4; DB 15; Length 1182;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 1148; Conservative 0; Mismatches 6; Indels 0;

QY	1	ATGAGCTCCCGGATCCAGATCTTCCGCGGGAGCGCGGCCCTACCTCTGGGCCCGAGCGCC	60
DB	14	ATGGAATCCCGGATTCAGATCTTCCGCGGGGAGCCTGGCCCTACCTCTGCGCCCGAGCGCC	73
QY	61	TGCGTGGCCCCCAACACGACGCGCTGGTTCTCCGGCTGGGCGGAGCCCGACGACGAACGCG	120
DB	74	TGCGTGGCCCCCAACACGACGCGCTGGTTCTCCGGCTGGGCGGAGCCCGACGACGAACGCG	133
QY	121	AGCGCCGGCTCGGAGGACGGCGAGCTGGAGCCCGCGCACATCTCCCCGGGCATCCCGGTC	180
DB	134	AGCGCGGCTCGGAGGACGGCGAGCTGGAGCCCGCGCACATCTCCCCGGGCATCCCGGTC	193
QY	181	ATCATCAGCGGGTCTACTCCGTAGTGTTTCTGCTGGGCTTGGTGGGCAACTCGCTGGTC	240
DB	194	ATCATCAGCGGGTCTACTCCGTAGTGTTTCTGCTGGGCTTGGTGGGCAACTCGCTGGTC	253
QY	241	ATGTTCTGTGATCATCCGATACACAAAGATCAAGACAGCAACCAACATTTACATATTTAAC	300
DB	254	ATGTTCTGTGATCATCCGATACACAAAGATCAAGACAGCAACCAACATTTACATATTTAAC	313
QY	301	CTGGCTTTGGCAGATGCTTTTAGTTACTACAAACCATGCCCCTTCAGAGTAGCGTCTACTTG	360
DB	314	CTGGCTTTGGCAGATGCTTTTAGTTACTACAAACCATGCCCCTTCAGAGTAGCGTCTACTTG	373
QY	361	ATGAATTCCTGGGCTTTTGGGATGTGCTGTGCAAGATAGTAATTTCCATGTGATCTAC	420
DB	374	ATGAATTCCTGGGCTTTTGGGATGTGCTGTGCAAGATAGTAATTTCCATGTGATCTAC	433
QY	421	AACATGTTCAACGACATCTTCACTTGACCATATGAGCGTGAGCCGCTACATTCGCGTG	480
DB	434	AACATGTTCAACGACATCTTCACTTGACCATATGAGCGTGAGCCGCTACATTCGCGTG	493
QY	481	TGCCACCCCGTGAAGGCTTTGGACTTTCCGCACACCCCTTGAAGGCAAGATCATCAATATC	540
DB	494	TGCCACCCCGTGAAGGCTTTGGACTTTCCGCACACCCCTTGAAGGCAAGATCATCAATATC	553
QY	541	TGCATCTGGTCTGTGCTGCATCTGTGTGGCATCTCTGCAATAGTCTCTTGAGGACACAAA	600
DB	554	TGCATCTGGTCTGTGCTGCATCTGTGTGGCATCTCTGCAATAGTCTCTTGAGGACACAAA	613
QY	601	GTCAAGGGAACGTCGATGTTCATTGATGTCTCTTCCAGTTCCTCCAGATGATGACTACTCC	660
DB	614	GTCAAGGGAACGTCGATGTTCATTGATGTCTCTTCCAGTTCCTCCAGATGATGACTACTCC	673
QY	661	TGCTGGGACCTCTTCATGAAGATCTGGCTCTTCATCTTTGCCCTTCGTGATCCCTGCTCTC	720
DB	674	TGCTGGGACCTCTTCATGAAGATCTGGCTCTTCATCTTTGCCCTTCGTGATCCCTGCTCTC	733
QY	721	ATCATCATGCTCTGTCTACACCTGTATGATCCTCGCTCTCAAGAGCGTCCGGCTCCTTTCT	780
DB	734	ATCATCATGCTCTGTCTACACCTGTATGATCCTCGCTCTCAAGAGCGTCCGGCTCCTTTCT	793
QY	781	GGCTCCGAGAGAAAGATCGCAACCTGCTGAGATCACAGACTGTGCTCTGTTGGTGGTG	840
DB	794	GGCTCCGAGAGAAAGATCGCAACCTGCTGAGATCACAGACTGTGCTCTGTTGGTGGTG	853
QY	841	GCAGTCTTCCTGCTCTGTGCGATCCCATTTCAATATTCATCTGTGGAGGCTCTGGGG	900
DB	854	GCGGTTTTCTGCTCTGTGCGATCCCATTTCAATATTCATCTGTGGAGGCTCTGGGG	913
QY	901	AGCACCTCCACAGCACAGCTGCTCTCTCAGCTATTTACTTTGCACTCGCCTTAGGCTAT	960
DB	914	AGCACCTCCACAGCACAGCTGCTCTCTCAGCTATTTACTTTGCACTCGCCTTAGGCTAT	973
QY	961	ACCAACAGTAGCCTGAATCCCATCTTCTACGCCCTTTCTTGATGAAATTTCAAGCGGTGT	1020
DB	974	ACCAACAGTAGCCTGAATCCCATCTTCTACGCCCTTTCTTGATGAAATTTCAAGCGGTGT	1033
QY	1021	TTCCGGGACTTCTGCTTTTCCACTGAAGATGAGGATGGAGCGGACAGCACTAGCAGATC	1080
DB	1034	TTCCGGGACTTCTGCTTTTCCACTGAAGATGAGGATGGAGCGGACAGCACTAGCAGATC	1093
QY	1081	CGAAATACAGTTCAGGATCCTGCTTACCTTGAGGACATCGATGGGATGAATAAACAGATA	1140



Db	1094	CGAAATACAGTTCAGGATCTGCTTACCTGAGGACATCGATGGATGAATAAACAGTA	1153
QY	1141	TGACTAGTCGTGGA	1154
Db	1154	TGACTAGTCGTGGA	1167
RESULT 12			
US-10-305-720-1417			
; Sequence 1417, Application US/10305720			
; Publication No. US20040010136A1			
; GENERAL INFORMATION:			
; APPLICANT: Au-Young, Janice K.; Seilbamer, Jeffrey J.			
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression			
; FILE REFERENCE: PA-0002-1 CON			
; CURRENT APPLICATION NUMBER: US/10/305,720			
; PRIORITY FILING DATE: 2002-11-26			
; PRIOR APPLICATION NUMBER: 09/016,434			
; PRIORITY FILING DATE: 1998-01-30			
; NUMBER OF SEQ ID NOS: 1490			
; SOFTWARE: PERL Program			
; SEQ ID NO 1417			
; LENGTH: 1182			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: misc feature			
; OTHER INFORMATION: GenBank ID No. US20040010136A1 9532059			
US-10-305-720-1417			
Query Match 99.2%; Score 1144.4; DB 17; Length 1182;			
Best Local Similarity 99.5%; Pred. No. 0;			
Matches 1148; Conservative 0; Mismatches 6; Indels 0; Gaps 0;			
QY	1	ATGGACTCCCCGATCCAGATCTTCCGCGGGAGCGCGGCTTACCTGCGCGCCGAGCGCC	60
Db	14	ATGGAATCCCGATTCCAGATCTTCCGCGGGAGCTTGGCCCTACCTGGCGCCCGAGCGCG	73
QY	61	TGCTGCCCCCAACAGCAGCGCTGTTCCGCGCTGGCGCGAGCCGACGACGACGCGC	120
Db	74	TGCTGCCCCCAACAGCAGCGCTGTTCCGCGCTGGCGCGAGCCGACGACGACGCGC	133
QY	121	AGCGCGGCTCGGAGGACGCGAGCTGGAGCGCGGCATCTCCCGCGCCATCCCGGTC	180
Db	134	AGCGCGGCTCGGAGGACGCGAGCTGGAGCGCGGCATCTCCCGCGCCATCCCGGTC	193
QY	181	ATCATCAGCGCGCTCTACTCCGTTAGTGTTCGTTGGGTTGGTGGGCAACTCGCTGGTC	240
Db	194	ATCATCAGCGCGCTCTACTCCGTTAGTGTTCGTTGGGTTGGTGGGCAACTCGCTGGTC	253
QY	241	ATGTTGTTGATATCCGATACAAAGATGAAGACGACGACCAACCAATTTACATATTAAC	300
Db	254	ATGTTGTTGATATCCGATACAAAGATGAAGACGACGACCAACCAATTTACATATTAAC	313
QY	301	CTGCTTTGTCAGATGCTTTAGTTACTACAAACATGCGCTTTCCAGAGTACGGTCTACTTG	360
Db	314	CTGCTTTGTCAGATGCTTTAGTTACTACAAACATGCGCTTTCCAGAGTACGGTCTACTTG	373
QY	361	ATGAATTCCTGGCTTTTGGGATGTCGTGCAAGATAGTAATTTCCATTTGATTAATAC	420
Db	374	ATGAATTCCTGGCTTTTGGGATGTCGTGCAAGATAGTAATTTCCATTTGATTAATAC	433
QY	421	AACATGTTACACGATCTTTCACCTTACCATGATGAGCGTGACCGCTACATTTGCCGTG	480
Db	434	AACATGTTACACGATCTTTCACCTTACCATGATGAGCGTGACCGCTACATTTGCCGTG	493
QY	481	TGCACCCCGTGAAGGCTTTGGACTTCCGACACCCCTTGAAGGCAAGATCATCAATATC	540
Db	494	TGCACCCCGTGAAGGCTTTGGACTTCCGACACCCCTTGAAGGCAAGATCATCAATATC	553
QY	541	TGATCTGGCTGCTGCTCATCTGTTGGATCTCTGCAATAGTCTTGGAGGACCAAA	600

RESULT 13  
US-10-283-975A-80  
; Sequence 80, Application US/10283975A  
; Publication No. US20040110792A1  
; GENERAL INFORMATION:  
; APPLICANT: Ortho-Clinical Diagnostics, Inc.  
; TITLE OF INVENTION: Methods For Assessing and Treating Leukemia  
; FILE REFERENCE: CDS 293 PCT  
; CURRENT APPLICATION NUMBER: US/10/283,975A  
; CURRENT FILING DATE: 2002-10-30  
; PRIOR APPLICATION NUMBER: 60/340,938  
; PRIOR FILING DATE: 2001-10-30  
; PRIOR APPLICATION NUMBER: 60/338,997  
; PRIOR FILING DATE: 2001-10-30  
; PRIOR APPLICATION NUMBER: 60/340,081  
; PRIOR FILING DATE: 2001-10-30  
; PRIOR APPLICATION NUMBER: 60/341,012  
; PRIOR FILING DATE: 2001-10-30  
; NUMBER OF SEQ ID NOS: 900  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 80  
; LENGTH: 1182  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-10-283-975A-80

Query Match 99.2%; Score 1144.4; DB 18; Length 1182;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 1148; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGAGTCTCCCGATCCAGATCTTCGCGGGAGCGCGCCCTTACCTGCGCCCGAGCGCC 60  
DB 14 ATGGAATCCCGGATTCAGATCTTCGCGGGAGCGCCCTTACCTGCGCCCGAGCGCC 73  
QY 61 TGCCTGCCCCCAACAGCAGCGCTGTTCCCGGCTGGCGCGAGCGCGAGCAACGGC 120  
DB 74 TGCCTGCCCCCAACAGCAGCGCTGTTCCCGGCTGGCGCGAGCGCGAGCAACGGC 133  
QY 121 AGCGCGGCTCGAGGAGCGCAGCTGGAGCGCGGCACATCTCCCGCGCCATCCCGTTC 180  
DB 134 AGCGCGGCTCGAGGAGCGCAGCTGGAGCGCGGCACATCTCCCGCGCCATCCCGTTC 193  
QY 181 ATCATCAGCGGCTTACTCCGTAAGTGTTCGCGGCTGGTGGGCAACTCGCTGTC 240  
DB 194 ATCATCAGCGGCTTACTCCGTAAGTGTTCGCGGCTGGTGGGCAACTCGCTGTC 253  
QY 241 ATGTTCTGTCATCCGATACACAAAGATGAGACAGCAACCAATTTACATTTAAC 300  
DB 254 ATGTTCTGTCATCCGATACACAAAGATGAGACAGCAACCAATTTACATTTAAC 313  
QY 301 CTGGCTTTGGCAGATGCTTTAGTTACTACCAACCATGCCCTTTCAGAGTACGCTTACTTG 360  
DB 314 CTGGCTTTGGCAGATGCTTTAGTTACTACCAACCATGCCCTTTCAGAGTACGCTTACTTG 373  
QY 361 ATGAATCTCGCTTTGGGATGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420  
DB 374 ATGAATCTCGCTTTGGGATGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 433  
QY 421 AACATGTTCCAGCAGATCTTACCTTGACCATGATGAGCGGTGGACCGCTACATTGCCGTG 480  
DB 434 AACATGTTCCAGCAGATCTTACCTTGACCATGATGAGCGGTGGACCGCTACATTGCCGTG 493  
QY 481 TGCCACCCGCTGAAGGCTTTGAGCTTCGCGCACCCCTTGAAGGCAAGATCATCAATATC 540  
DB 494 TGCCACCCGCTGAAGGCTTTGAGCTTCGCGCACCCCTTGAAGGCAAGATCATCAATATC 553  
QY 541 TGCAATCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
DB 554 TGCAATCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 613  
QY 601 GTCCGGAAGAGCTGATGCTGATGAGTGTCTTGGAGTTCCTGCAATAGTCTTGGAGGACCAA 660  
DB 614 GTCCGGAAGAGCTGATGCTGATGAGTGTCTTGGAGTTCCTGCAATAGTCTTGGAGGACCAA 673  
QY 661 TGGTGGGACCTTCTCATGAAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720  
DB 674 TGGTGGGACCTTCTCATGAAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 733  
QY 721 ATCATCATCGTCTGCTACACCTGATGATCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 780  
DB 734 ATCATCATCGTCTGCTACACCTGATGATCTGCGTCTCAAGAGCGTCCGGCTCCTTTCT 793  
QY 781 GGCTCCGAGAGAAGATCGAACCCTGCTGATGAGTACACAGACTGCTGCTGCTGCTGCTGCTG 840  
DB 794 GGCTCCGAGAGAAGATCGAACCCTGCTGATGAGTACACAGACTGCTGCTGCTGCTGCTGCTG 853  
QY 841 GCAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
DB 854 GCGGTTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 913  
QY 901 AGCACCTCCACAGCAGCTGCTCTCTCCAGCTATTAATTTCTGATCGCTTCTAGGCTAT 960  
DB 914 AGCACCTCCACAGCAGCTGCTCTCTCCAGCTATTAATTTCTGATCGCTTCTAGGCTAT 973  
QY 961 ACCAACAGTACCTGAATCCATTTCTTACGCTTTCTTGTATGAATAATTTCAAGCGGTGT 1020  
DB 974 ACCAACAGTACCTGAATCCATTTCTTACGCTTTCTTGTATGAATAATTTCAAGCGGTGT 1033  
QY 1021 TTCCGGGACTTCTGCTTTCCACTGAGATGAGATGGAGCGGACAGCACTAGCAGATC 1080  
DB 1034 TTCCGGGACTTCTGCTTTCCACTGAGATGAGATGGAGCGGACAGCACTAGCAGATC 1093  
QY 1081 CGAAATACAGTTACGATCTTCTGCTTACCTGAGGAGACATCGATGGATGAATAAACCACTA 1140

DB 1094 CGAAATACAGTTACGATCTTCTGCTTACCTGAGGACATCGATGGATGAATAAACCACTA 1153  
QY 1141 TGACTAGTCGTGGA 1154  
DB 1154 TGACTAGTCGTGGA 1167

## RESULT 14

US-10-318-661-1  
; Sequence 1, Application US/10318661  
; Publication No. US20030167476A1  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Bruce R.  
; TITLE OF INVENTION: Selective Target Cell Activation By  
; TITLE OF INVENTION: Expression of A G Protein-Coupled Receptor Activated  
; TITLE OF INVENTION: Superiorly By Synthetic Ligand  
; FILE REFERENCE: UCAL-049CIP2  
; CURRENT APPLICATION NUMBER: US/10/318,661  
; CURRENT FILING DATE: 2003-05-05  
; PRIOR APPLICATION NUMBER: US 09/341,446  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: PCT/US97/05334  
; PRIOR FILING DATE: 1997-03-25  
; PRIOR APPLICATION NUMBER: US 08/622,348  
; PRIOR FILING DATE: 1996-03-26  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1143  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-318-661-1

Query Match 98.9%; Score 1141.4; DB 16; Length 1143;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1142; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAGTCTCCCGATCCAGATCTTCGCGGGAGCGCGCCCTTACCTGCGCCCGAGCGCC 60  
DB 1 ATGAGTCTCCCGATCCAGATCTTCGCGGGAGCGCGCCCTTACCTGCGCCCGAGCGCC 60  
QY 61 TGCCTGCCCCCAACAGCAGCGCTGTTCCCGGCTGGCGCGAGCGCGAGCAACGGC 120  
DB 61 TGCCTGCCCCCAACAGCAGCGCTGTTCCCGGCTGGCGCGAGCGCGAGCAACGGC 120  
QY 121 AGCGCGGCTCGAGGAGCGCAGCTGGAGCGCGGCACATCTCCCGCGCCATCCCGTTC 180  
DB 121 AGCGCGGCTCGAGGAGCGCAGCTGGAGCGCGGCACATCTCCCGCGCCATCCCGTTC 180  
QY 181 ATCATCAGCGGCTTACTCCGTAAGTGTTCGCTGCTGGCTTGGTGGGCAACTCGCTGTC 240  
DB 181 ATCATCAGCGGCTTACTCCGTAAGTGTTCGCTGCTGGCTTGGTGGGCAACTCGCTGTC 240  
QY 241 ATGTTCTGTCATCCGATACACAAAGATGAGACAGCAACCAATTTACATTTAAC 300  
DB 241 ATGTTCTGTCATCCGATACACAAAGATGAGACAGCAACCAATTTACATTTAAC 300  
QY 301 CTGGCTTTGGCAGATGCTTTAGTTACTACCAACCATGCCCTTTCAGAGTACGCTTACTTG 360  
DB 301 CTGGCTTTGGCAGATGCTTTAGTTACTACCAACCATGCCCTTTCAGAGTACGCTTACTTG 360  
QY 361 ATGAATCTCGCTTTGGGATGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420  
DB 361 ATGAATCTCGCTTTGGGATGCTGTGCAAGATAGTAATTTCCATTGATTACTAC 420  
QY 421 AACATGTTCCAGCAGATCTTACCTTGACCATGATGAGCGGTGGACCGCTACATTGCCGTG 480  
DB 421 AACATGTTCCAGCAGATCTTACCTTGACCATGATGAGCGGTGGACCGCTACATTGCCGTG 480  
QY 481 TGCCACCCGCTGAAGGCTTTGAGCTTCGCGCACCCCTTGAAGGCAAGATCATCAATATC 540  
DB 481 TGCCACCCGCTGAAGGCTTTGAGCTTCGCGCACCCCTTGAAGGCAAGATCATCAATATC 540



Qy	1022	TCGGGACITTCGCTTTC	CACTG	AGATG	AGGAT	TGGAG	CGGCA	GAGCA	CTAG	CAGAGTCC	1081
Db	1133	TCGGGACITTCGCTTTC	CACTG	AGATG	AGGAT	TGGAG	CGGCA	GAGCA	CTAG	CAGAGTCC	1192
Qy	1082	GAATACAGTTCAGGATCCT	TACCT	CCTGAGG	ACATCG	GATGG	GAATG	GAAT	TAAC	CAAGTAT	1141
Db	1193	GAATACAGTTCAGGATCCT	TACCT	CCTGAGG	ACATCG	GATGG	GAATG	GAAT	TAAC	CAAGTAG	1252
Qy	1142	G	1142								
Db	1253	G	1253								

Search completed: April 6, 2005, 13:18:10  
Job time : 769.333 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 6, 2005, 12:28:42 ; Search time 4384.33 Seconds  
(without alignments)  
10018.893 Million cell updates/sec

Title: US-09-904-584-4

Perfect score: 1154

Sequence: 1 atggactcccgatccagat.....ccagatgactagtcgtgga 1154

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*

- 1: gb\_est1:\*
- 2: gb\_est2:\*
- 3: gb\_hc:\*
- 4: gb\_est3:\*
- 5: gb\_est4:\*
- 6: gb\_est5:\*
- 7: gb\_est6:\*
- 8: gb\_gss1:\*
- 9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	805.2	69.8	895	6	CB565888
2	581.8	50.4	762	7	CO960667
3	518.8	45.0	784	7	CO960682
4	470.6	40.8	837	7	CF593603
5	466.4	40.4	480	5	BX092912
6	429.2	37.2	2405	3	AK038389
7	418.4	36.3	4022	3	AK043873
8	366.2	31.7	2919	3	AK038620
9	366.2	31.7	2959	3	AK079529
10	350.4	30.4	879	9	AY410745
11	334	28.9	2940	3	AK044178
12	325.8	28.2	2974	3	AK043275
13	325.4	28.2	3101	3	AK031926
14	324.2	28.1	879	9	AY410747
15	309.8	26.8	1053	9	CNS04C2T
16	277.6	24.1	775	5	BX874804
17	274.2	23.8	787	7	CN439929
18	270.2	23.4	917	5	BX219878
19	269.8	23.4	888	2	BF676176
20	264.4	22.9	579	5	BP214141
21	263.8	22.9	579	5	BP213719
22	239.8	20.8	657	2	BB588668
23	229.6	19.9	682	9	AY410746
24	228	19.8	1176	9	AY400827

25	227.4	19.7	389	2	BE649947
26	225	19.5	1176	9	AY400829
27	225	19.5	2014	3	AK046464
28	224.6	19.5	980	4	BM543468
29	223	19.3	632	2	BB641725
30	219.8	19.0	1006	9	AY400676
31	216	18.7	784	5	BQ179053
32	215.8	18.7	750	7	CO934661
33	214	18.5	429	4	BM342951
34	213.2	18.5	1006	9	AY400674
35	213.2	18.5	2048	3	CR593522
36	213	18.5	836	9	CNS0261
37	213	18.5	866	6	CD246184
38	212.2	18.4	2432	3	AK051189
39	211	18.3	531	9	CE517843
40	208.6	18.1	877	9	CNS028C2
41	206.6	17.9	842	9	CNS028KU
42	206.4	17.9	672	7	CO957761
43	206.2	17.9	697	5	BUI39251
44	206.2	17.9	757	5	BUI614716
45	203.4	17.6	785	4	BI754749

ALIGNMENTS

RESULT 1  
LOCUS CB565888  
DEFINITION AGENCOURT 12691503 NIH MGC 146 Homo sapiens cDNA clone  
IMAGE:6519213 5', mRNA sequence.  
ACCESSION CB565888  
VERSION CB565888.1 GI:29485418  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 895)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)  
Tissue Procurement: Guthrie cDNA Resource Center  
cDNA Library Preparation: Guthrie cDNA Resource Center  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: IRBF001 row: f column: 09  
High quality sequence stop: 763.  
Location/Qualifiers  
1. .895  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clones="IMAGE:6519213"  
/tissue\_type="mixed"  
/lab\_host="DH10B (TI-phage-resistant)"  
/clone\_lib="NIH MGC 146"  
/notes="Vector: pCDNA3.1; Site 1: multiple; Site 2: multiple; ORF's were PCR-amplified (from IMAGE clones or from commercially available cDNA libraries) and cloned by the Guthrie cDNA Resource Center ([www.guthrie.org/cDNA](http://www.guthrie.org/cDNA)) into pCDNA3.1. For specific information on cloning sites (which vary by clone), please refer to the Guthrie website, using the Guthrie ID given in the file <ftp://image.llnl.gov/images-rearranged/plates/IRBF.presv.dat>  
a. Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 69.8%; Score 805.2; DB 6; Length 895;  
 Best Local Similarity 97.1%; Pred. No. 2.1e-200;  
 Matches 841; Conservative 0; Mismatches 23; Indels 2; Gaps 2;

QY 1 ATGGATCTCCCGATCCAGATCTTCCGCGGGAGCCGGCCCTACCTGCGCCCGAGCGCC 60  
 DB 2 ATGGAATCCCGATTCAGATCTTCCGCGGGAGCCGGCCCTACCTGCGCCCGAGCGCC 61

QY 61 TGCCTGCCCGCCCAACAGCAGCGCTGTTTCCGGCTGGCGGAGCCCGACAGCAACGGC 120  
 DB 62 TGCCTGCCCGCCCAACAGCAGCGCTGTTTCCGGCTGGCGGAGCCCGACAGCAACGGC 121

QY 121 AGCGCGGCTCGAGGACGCGCAGCTGGAGCCCGCGCACATCTCCCGCGCCATCCCGGTC 180  
 DB 122 AGCGCGGCTCGAGGACGCGCAGCTGGAGCCCGCGCACATCTCCCGCGCCATCCCGGTC 181

QY 181 ATCATCACGCGGCTTACTCCGAGTGTGCTGCTGGGCTTGGTGGCAACTCGCTGGTC 240  
 DB 182 ATCATCACGCGGCTTACTCCGAGTGTGCTGCTGGGCTTGGTGGCAACTCGCTGGTC 241

QY 241 ATGTTCTGATCATCCGATACACAGATGAAGACAGCAACCAACATTTACATATTAAAC 300  
 DB 242 ATGTTCTGATCATCCGATACACAGATGAAGACAGCAACCAACATTTACATATTAAAC 301

QY 301 CTGCGCTTTGGCAGATGCTTTAGTTACTACCAACCATGCCCTTTCCAGAGTACGGTCTACTTG 360  
 DB 302 CTGCGCTTTGGCAGATGCTTTAGTTACTACCAACCATGCCCTTTCCAGAGTACGGTCTACTTG 361

QY 361 ATGAATCTCTGGCTTTGGGAGATGCTGTGCAAGATAGTAATTTCCATTTGATTACTAC 420  
 DB 362 ATGAATCTCTGGCTTTGGGAGATGCTGTGCAAGATAGTAATTTCCATTTGATTACTAC 421

QY 421 AACATGTTACACAGCATCTTCACTTTGACCATGATGAGGTGACCGCTACATTTGCCGTC 480  
 DB 422 AACATGTTACACAGCATCTTCACTTTGACCATGATGAGGTGACCGCTACATTTGCCGTC 481

QY 481 TGCCACCCCGTGAAGGCTTTGGACTTCCGACACACCCCTTGAAGCAAGATCATCAATATC 540  
 DB 482 TGCCACCCCGTGAAGGCTTTGGACTTCCGACACACCCCTTGAAGCAAGATCATCAATATC 541

QY 541 TGCAATCTGGCTGTGCTGTCATCTGTTGGATCTCTGCAATAGTCTCTTGAGGACACAAA 600  
 DB 542 TGCAATCTGGCTGTGCTGTCATCTGTTGGATCTCTGCAATAGTCTCTTGAGGACACAAA 601

QY 601 GTCCAGGAGACCTCCGATGTCATTGAGTGTCTCTGAGTTCCTCCAGATGATGACTACTCC 660  
 DB 602 GTCCAGGAGACCTCCGATGTCATTGAGTGTCTCTGAGTTCCTCCAGATGATGACTACTCC 661

QY 661 TGGTGGGACCTCTTATGAAGATCTGCTGCTTCTCATCTTTGCTTCCGTGATCCCTGTCCTC 720  
 DB 662 TGGTGGGACCTCTTATGAAGATCTGCTGCTTCTCATCTTTGCTTCCGTGATCCCTGTCCTC 721

QY 721 ATCATCATGCTGTGTACACCTGATGATCTCGGCTCTCAAGAGCGTCC-GGCTCTCTTTC 779  
 DB 722 ATCATCATGCTGTGTACACCTGATGATCTCGGCTCTCAAGAGCGTCCGGGCTCTCTTTC 781

QY 780 TGGCTCCCGAGAGAGATC-GCAACTGCTGAGGATCACCAGCTGCTCTGCTGCTGCTG 838  
 DB 782 TGGCTCCCGAGAGAGATCNGCACCTGCTGAGGATCACCAGCTGCTCTGCTGCTGCTG 841

QY 839 TGGCAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 864  
 DB 842 GTGGGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 867

RESULT 2  
 CO960667  
 LOCUS  
 DEFINITION AGENCOURT 30842630 NIH MGC 146 Homo sapiens cDNA clone  
 IMAGE:7389810 5', mRNA sequence.  
 ACCESSION CO960667  
 VERSION CO960667.1 GI:51325223  
 KEYWORDS EST.

SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 REFERENCE 1 (bases 1 to 762)  
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: gcnbs-remail.nih.gov  
 Tissue Procurement: Guthrie cDNA Resource Center  
 cDNA Library Preparation: Guthrie cDNA Resource Center  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: IRB18 row: d column: 04  
 High quality sequence start: 30  
 High quality sequence stop: 549.  
 Location/Qualifiers  
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 /db\_xref="taxon:9606"  
 /clone="IMAGE:7389810"  
 /lab\_host="DH10B (T1-phage-resistant)"  
 /clone\_lib="NIH MGC 146"  
 /note="Vector: pCDNA3.1; Site 1: multiple; Site 2:  
 multiple; ORF's were PCR-amplified (from IMAGE Clones or  
 from commercially available cDNA libraries) and cloned by  
 the Guthrie cDNA Resource Center (www.guthrie.org/cDNA)  
 into pCDNA3.1. For specific information on cloning sites  
 (which vary by clone), please refer to the Guthrie  
 website, using the Guthrie ID given in the file  
 ftp://image.llnl.gov/image.rearrayed\_plates/IRBF.presv.dat  
 a. Note: this is a NIH\_MGC Library."

# ORIGIN

Query Match 50.4%; Score 581.8; DB 7; Length 762;  
 Best Local Similarity 97.1%; Pred. No. 1.2e-141;  
 Matches 603; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

QY 1 ATGGATCTCCCGATCCAGATCTTCCGCGGGAGCCGGCCCTACCTGCGCCCGAGCGCC 60  
 DB 27 ATGGAATCCCGATTCAGATCTTCCGCGGGAGCCGGCCCTACCTGCGCCCGAGCGCC 86

QY 61 TGCCTGCCCGCCCAACAGCAGCGCTGTTTCCGGCTGGCGGAGCCCGACAGCAACGGC 120  
 DB 87 TGCCTGCCCGCCCAACAGCAGCGCTGTTTCCGGCTGGCGGAGCCCGACAGCAACGGC 146

QY 121 AGCGCGGCTCGAGGACGCGCAGCTGGAGCCCGCGCACATCTCCCGCGCCATCCCGGTC 180  
 DB 147 AGCGCGGCTCGAGGACGCGCAGCTGGAGCCCGCGCACATCTCCCGCGCCATCCCGGTC 206

QY 181 ATCATCACGCGGCTTACTCCGAGTGTGCTGCTGGGCTTGGTGGCAACTCGCTGGTC 240  
 DB 207 ATCATCACGCGGCTTACTCCGAGTGTGCTGCTGGGCTTGGTGGCAACTCGCTGGTC 266

QY 241 ATGTTCTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTAAAC 300  
 DB 267 ATGTTCTGATCATCCGATACACAAAGATGAAGACAGCAACCAACATTTACATATTAAAC 326

QY 301 CTGGCTTTGGCAGATGCTTTAGTTACTACCAACCATGCCCTTTCCAGAGTACGGTCTACTTG 360  
 DB 327 CTGGCTTTGGCAGATGCTTTAGTTACTACCAACCATGCCCTTTCCAGAGTACGGTCTACTTG 386

QY 361 ATGAATCTCTGGCTTTTGGGAGTGTGCTGCAAGATAGTAATTTCCATTTGATTACTAC 420



Db 387 ATGATTCCTGGCCTTTTGGGATGCTGTGCAAGATAGTAATTTCAATTGATTACTAC 446  
 Qy 421 AACATGTTCCACGACATCTTACCTTGACCATGATGAGCGTGAGCCGCTACATTTGCCGTG 480  
 Db 447 AACATGTTCCACGACATCTTACCTTGACCATGATGAGCGTGAGCCGCTACATTTGCCGTG 506  
 Qy 481 TGCCACCCCGTGAAGGCTTTGGACCTCCGACACACCTTGAAGGCAAGATCATCAATATC 540  
 Db 507 TGCCACCCCGTGAAGGCTTTGGACCTCCGACACACCTTGAAGGCAAGATCATCAATATC 566  
 Qy 541 TGCATCTGGCT-GCTGTGCTCATCTGTTGGCATCTCTGCAATAGTCCCTTTGGAGGACCA 599  
 Db 567 TGCATCTGGCTGGCTGTGCTCATCTGTTAGCATCTCTGCTATATCTCTTGGGAGCGCA 626  
 Qy 600 AGTCAGGAAGACGTCGATGT 620  
 Db 627 AATCAGGAAGACTCGAAGT 647

RESULT 3  
 CO960682/c  
 LOCUS  
 DEFINITION AGNCOURT 30842262 NIH MGC 146 Homo sapiens cDNA clone  
 IMAGE:7389810 3', mRNA sequence.

ACCESSION  
 VERSION CO960682.1 GI:51325238  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Guthrie cDNA Resource Center  
 cDNA Library Preparation: Guthrie cDNA Resource Center  
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
 Clone Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: IRB18 row: d column: 04  
 High quality sequence start: 214  
 High quality sequence stop: 494.  
 Location/Qualifiers

1. 784  
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 /note="Vector: pCDNA3.1; Site 1: multiple; Site 2:  
 multiple; ORF's were PCR-amplified from IMAGE clones or  
 from commercially available cDNA libraries) and cloned by  
 the Guthrie cDNA Resource Center (www.guthrie.org/cDNA)  
 into pCDNA3.1. For specific information on cloning sites  
 (which vary by clone), please refer to the Guthrie  
 website, using the Guthrie ID given in the file  
 ftp://image.llnl.gov/image.rearrayed\_plates/IRBF.presv.dat  
 a. Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 45.0%; Score 518.8; DB 7; Length 784;  
 Best Local Similarity 97.6%; Pred. No. 4.3e-125;  
 Matches 537; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Qy 586 CTTGGAGGCAACAAAGTCAGGAAAGACGTGATGTCATTGAGTCTCTTTCAGTTCCTCA 645  
 Db 577 CTTGGAGGCAACAAAGTCAGGAAAGACGTGATGTCATTGAGTCTCTTTCAGTTCCTCA 519  
 Qy 646 GATGATGACTACTCTCTGGTGGGACCTTTCATGAGATCTGGCTTTCATCTTTGCCCTTC 705  
 Db 518 GATGATGACTACTCTCTGGTGGGACCTTTCATGAGATCTGGCTTTCATCTTTGCCCTTC 459  
 Qy 706 GTGATCCCTGTCCTCATCATCATCTGCTGTACACCCCTGATGATCTCTGCGTCTCAAGAGC 765  
 Db 458 GTGATCCCTGTCCTCATCATCATCTGCTGTACACCCCTGATGATCTCTGCGTCTCAAGAGC 399  
 Qy 766 GTCCGGCTCTCTTCTGGCTCCCGAGAGAAAGATCGCAACCTGCTAGGATCACCAGACTG 825  
 Db 398 GTCCGGCTCTCTTCTGGCTCCCGAGAGAAAGATCGCAACCTGCTAGGATCACCAGACTG 339  
 Qy 826 GTCTCTGGTGGTGGGAGCTTCTGCTGTCTGGAGTCCCATTCATCATATTCATCTCTG 885  
 Db 338 GTCTCTGGTGGTGGGAGCTTCTGCTGTCTGGAGTCCCATTCATCATATTCATCTCTG 279  
 Qy 886 GTGGAGGCTCTGGGAGGACCTCCACAGACAGCTGCTCTCTCAGCTATTACTTTCTGTC 945  
 Db 278 GTGGAGGCTCTGGGAGGACCTCCACAGACAGCTGCTCTCTCAGCTATTACTTTCTGTC 219  
 Qy 946 ATGCGCTTAGGCTATACCAACAGTAGCTGAATCCCATTTCTCTACGCTTTTCTTTGATGAA 1005  
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RESULT 4

CF593603

LOCUS

DEFINITION

AGNCOURT 15623822 NIH MGC 147 Homo sapiens cDNA clone

IMAGE:30531690 5', mRNA sequence.

ACCESSION

CF593603

VERSION

CF593603.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC http://mgi.nci.nih.gov/

1 (bases 1 to 837)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Stefan Hanson

cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help

and advice from Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: NDAM622 row: n column: 19

High quality sequence stop: 592.



RESULT 6	AK038389	2405 bp	linear	HTC 03-APR-2004
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DEFINITION	Mus musculus adult male hypothalamus cDNA, RIKEN full-length enriched library, clone:A230002D02 product:opioid receptor, mu, full insert sequence.			
ACCESSION	AK038389			
VERSION	AK038389.1	GI:26332528		
KEYWORDS	HTC; CAP trapper.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Carninci, P. and Hayashizaki, Y.			
AUTHORS	Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.			
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes			
JOURNAL	Genome Res.	10 (10), 1617-1630	(2000)	
MEDLINE	20499374			
PUBMED	11042159			
REFERENCE	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.			
AUTHORS	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer			
TITLE	Genome Res.	10 (11), 1757-1771	(2000)	
JOURNAL	20530913			
MEDLINE	11076861			
PUBMED				
REFERENCE	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.			
AUTHORS	Functional annotation of a full-length mouse cDNA collection			
TITLE	Nature	409, 685-690	(2001)	
JOURNAL				
REFERENCE	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.			
AUTHORS	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs			
TITLE	Nature	420, 563-573	(2002)	
JOURNAL				
REFERENCE	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saiki, R., Saichoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.			
AUTHORS	Direct Submission			
TITLE	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp).			
JOURNAL				
REFERENCE	URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,			
AUTHORS				

COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/.			
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RESULT 7
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DEFINITION Mus musculus 10 days neonate cortex cDNA, RIKEN full-length
RECEPTOR, full insert sequence.
ACCESSION AK043873
VERSION AK043873.1 GI:26335979
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
REFERENCE
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
2
REFERENCE
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
3
REFERENCE
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,
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TITLE The RIKEN Genome Exploration Research Group Phase II Team and the
JOURNAL FANTOM Consortium.
MEDLINE Functional annotation of a full-length mouse cDNA collection
PUBMED Nature 409, 685-690 (2001)
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
TITLE The FANTOM Consortium and the RIKEN Genome Exploration Research
JOURNAL Analysis of the mouse transcriptome based on functional annotation
REFERENCE of 60,770 full-length cDNAs
AUTHORS Nature 420, 563-573 (2002)
6 (bases 1 to 4022)
TITLE Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
JOURNAL Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
REFERENCE Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
AUTHORS Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
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Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
FEATURES
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sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

20530913

11076861

#### REFERENCE

#### AUTHORS

The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection

Nature 409, 685-690 (2001)

5

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 2959)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,

Fukuda, S., Furuno, M., Hangaki, T., Hara, A., Hashizume, W.,

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Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,

Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of

Physical and Chemical Research (RIKEN), Laboratory for Genome

Exploration Research Group, RIKEN Genomic Sciences Center (GSC),

RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,

Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,

URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222,

Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.

Please visit our web site for further details.

URL: <http://genome.gsc.riken.jp/>

URL: <http://fantom.gsc.riken.jp/>.

#### FEATURES

##### source

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Db 401 GGGGGGCTCTCGGGAACTGCTCGTATGTCATCTCTCAGGCACACCAAGATGAAG 460

Qy 274 ACAGCAACCAACATTTACATATTTAACTGGCTTTGGCAGATGCTTTAGTTACTACACC 333

Db 461 ACTGCTACCAACATTTACATATTTAACTGGCCTTCTGGCCATTCCTGGTCTTGTGACA 520

Qy 334 ATGCCCTTTTCAGAGTACGGTCTACTTCATGAATTCCTGGCCCTTTTGGGATGTGTGTGC 393

Db 521 CTGCCCTTCCAGGCACAGACATCTTCTGGGCTTCTGGCCATTTGGGAATGCATGTGC 580

Qy 394 AAGATAGTAATTTCCATTGATTTACTACAACATGTTCCACAGCATCTTCACCTTGACCAATG 453

Db 581 AAGACGGTCAATTGCTATCGACTACTACAACATGTTTACCAGCACTTTTCACTTTGACTGCC 640

Qy 454 ATGACGCTGGACCGCTACATTTGCGTGTGTCACCCCGTGAAGGCTTTGGACTTCGGACA 513

Db 641 ATGAGTGTAGACCGCTTATAGCTATTCGCCACCTTATCGTGGCCTTGTATGTTGGGACA 700

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Db 1232 CGGAGATGACAGGTTTCTGATCTGCTGCGCAGCATTGCCAAGGAT 1276

polyA\_signal



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RESULT 10
LOCUS AY410745
DEFINITION Homo sapiens OPRL1 gene, 879 bp DNA linear GSS 16-DEC-2003
genomic survey sequence.
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VERSION AY410745.1 GI:39766713
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 879)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarilwal,A.,
Todd,M.A., Tanenbaum,D.M., Civeillo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 879)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarilwal,A.,
Todd,M.A., Tanenbaum,D.M., Civeillo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Mus musculus 10 days neonate cortex cDNA, RIKEN full-length
enriched library, clone:A830097K10 product:NOICEPIN RECEPTOR
(OEPANIN FQ RECEPTOR), full insert sequence.
AK044178
VERSION AK044178.1 GI:26090219
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20493374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsumai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohata,E., Watahiki,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection

```

JOURNAL REFERENCE	Nature 409, 685-690 (2001)	Qy	315	TGCTTTAGTTACTACAAACCATGCCCTTTTCAGAGTACGGTCTTACTTGATGAATTCCTGGCC	374
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.	Db	483	TACCTGGTCTTGCTGACACTGCCCTTCCAGGGCACAGACATCTCTTCTGGGCTTCTGGCC	542
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs	Qy	375	TTTTGGGATGTGTGTGCAAGATAGTAATTTCCATTGATTACTACAACATGTTTCACAG	434
JOURNAL REFERENCE	Nature 420, 563-573 (2002)	Db	543	ATTTGGGAATGCATGTGCAAGACGGTCATTGTCTATCGACTACTACAACATGTTTACCAG	602
AUTHORS	6 (bases 1 to 2940)	Qy	435	CATCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTCGCGTGTGCCACCCGCGTAA	494
	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Segabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.	Db	603	CACCTTCACCTTGACCATGATGAGCGTGGACCGTATGTAGCTATCTGCCACCTATCCG	662
	Direct Submission	Qy	495	GGCTTTGGACTTCGCGACACCCCTTTGAAGGCAAAAGATCATCAATATCTGCATCTGCGTCT	554
TITLE	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)	Db	663	TGCCCTTTGATGTTTCGGACATCCAGTAAAGCCGCGCTTAATGTGGCCATATGGCCCT	722
JOURNAL REFERENCE	Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.	Qy	555	GTCTGTCATCTGTGGCATCTCTGCAATAGTCTTGGAGGACCAAGTCAGGGAGAGAGT	614
AUTHORS	Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/	Db	723	GGCTTCGGTGTGTGTCTCTGCTTGGCATCATGGGCTCAGCACAAAGT-----GGAGGA	776
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 AK043275  
 ACCESSION  
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 HTG; CAP trapper.  
 KEYWORDS  
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 AUTHORS  
 Carninci, P. and Hayashizaki, Y.



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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
 1  
 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,  
 Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
 TITLE  
 High-efficiency full-length cDNA cloning  
 JOURNAL  
 Meth. Enzymol. 303, 19-44 (1999)  
 MEDLINE  
 99279253  
 PUBMED  
 10349636

REFERENCE  
 2  
 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,  
 Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
 TITLE  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes  
 JOURNAL  
 Genome Res. 10 (10), 1617-1630 (2000)  
 MEDLINE  
 20499374  
 PUBMED  
 11042159

REFERENCE  
 3  
 Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,  
 Konno,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M.,  
 Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,  
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 Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,  
 Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,  
 Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
 TITLE  
 RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer  
 JOURNAL  
 Genome Res. 10 (11), 1757-1771 (2000)  
 MEDLINE  
 20530913  
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 11076861

REFERENCE  
 4  
 The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 TITLE  
 Functional annotation of a full-length mouse cDNA collection  
 JOURNAL  
 Nature 409, 685-690 (2001)  
 MEDLINE  
 11076861

REFERENCE  
 5  
 The FANTOM Consortium and the RIKEN Genome Exploration Research  
 Group Phase I & II Team.  
 TITLE  
 Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 JOURNAL  
 Nature 420, 563-573 (2002)  
 MEDLINE  
 11076861

REFERENCE  
 6  
 (bases 1 to 3101)  
 Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,  
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 Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,  
 Muramatsu,M. and Hayashizaki,Y.  
 TITLE  
 Direct Submission  
 JOURNAL  
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome

COMMENT  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
 Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp,  
 URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,  
 Fax:81-45-503-9216)  
 cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedic Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Please visit our web site for further details.  
 URL:http://genome.gsc.riken.jp/  
 URL:http://fantom.gsc.riken.jp/.

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AUTHORS Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.  
TITLE Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence  
JOURNAL Nat. Genet. 25 (2), 235-238 (2000)  
MEDLINE 20296633  
PUBMED 10835645  
REFERENCE 2  
AUTHORS Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C., Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.  
TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis  
JOURNAL Genome Res. 10 (7), 939-949 (2000)  
MEDLINE 20359837  
PUBMED 10899143  
REFERENCE 3 (bases 1 to 1053)  
AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)  
COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/tetraodon.  
FEATURES Location/Qualifiers  
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Matches 587; Conservative 8; Mismatches 230; Indels 74; Gaps 7;  
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